

Best Available Copy

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OM protein - protein search, using sw model

Run on: January 10, 2006, 22:59:27 ; Search time 136 Seconds
 (without alignments)
 481.378 Million cell updates/sec

Title: AAH26175
 Perfect score: 776
 Sequence: 1 mkfklhvnsargykkd1wnms.....psptssstvtqapsrrpiv 149.

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_GeneSeq_21;*

- 1: geneseqp1980s;*
- 2: geneseqp1990s;*
- 3: geneseqp2000s;*
- 4: geneseqp2001s;*
- 5: geneseqp2002s;*
- 6: geneseqp2003aa;*
- 7: geneseqp2003bb;*
- 8: geneseqp2004s;*
- 9: geneseqp2005s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	651.5	84.0	482	8 ADR10403	Adr10403 Human pro Adv0585 Human ATF
2	636	82.0	487	9 ADV50585	Adv0585 Human ATF
3	439	56.6	411	5 ABB57020	Abb57020 Mouse isc
4	300	38.7	413	8 ADP80860	Adp80860 Mouse C13
5	260.5	33.6	501	7 ADC18733	Adc18733 Human cyc
6	212	27.3	52	3 AAG02942	Aag02942 Human sec
7	137	17.7	29	4 AAB68325	Aab68325 c-Jun ami
8	137	17.7	29	7 PDF17325	Adf17325 Synthetic
9	137	17.7	29	8 ADO01349	Ado01349 c-Jun ami
10	109.5	14.2	1483	8 ADQ97206	Adq97206 Mouse can
11	109	14.0	364	5 AAE18363	Aae18363 Streptoco
12	109	14.0	389	5 ABP25889	Abp25889 Streptoco
13	109	14.0	389	5 AAE18359	Aae18359 Streptoco
14	109	14.0	389	8 ADR83905	Adr83905 S. Pyogen
15	109	14.0	447	3 AAB14349	Aab14349 Human Zic
16	109	14.0	447	8 ADN04236	Adn04236 Anti-psori
17	109	14.0	447	8 ADQ17360	Adq17360 Human sof
18	109	14.0	1027	7 BBM85538	Abm85538 Mouse pro
19	108	13.9	447	8 ADU18114	Adu18114 Human ost
20	107	13.8	447	5 ABB57042	Abb57042 Mouse isc
21	106.5	13.7	97	4 BAB62172	Aab62172 Zinc fing
22	106.5	13.7	97	1 AAE28179	Aae28179 Zinc fing
23	106.5	13.7	97	9 ADX4497	Adx4497 Zinc fing
24	105.5	13.6	297	2 AAW08955	Aaw08955 Chimeric

ALIGNMENTS

RESULT 1
 ADR10403
 ID ADR10403 standard; protein; 482 AA.
 XX
 AC ADR10403;
 XX
 DT 04-NOV-2004 (First entry)

XX Human protein useful for treating neurological disease Seq 3909.
 XX human; oligo-capping method; diagnostic marker; gene therapy;
 XX osteoporosis; neurological disease; Alzheimer's disease;
 XX Parkinson's disease; dementia; short memory; cancer;
 XX sense or motor function; emotional reaction; fear response; panic;
 XX osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
 XX tranquiliser.
 XX Homo sapiens.
 XX
 PN EPI447413-A2.
 XX
 PD 18-AUG-2004.
 XX
 PR 12-FEB-2004; 2004BP-00003145.
 XX
 PR 14-FEB-2003; 2003JP-00102207.
 XX
 PR 09-MAY-2003; 2003JP-00131452.
 XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
 PI Wakamatsu A, Ishii S, Nagai K, Irie R;
 XX
 DR WPI; 2004-582265/57.
 DR N-PSDB; ADR08447.

XX
 PS Claim 1; SEQ ID NO 3909; 2686pp; English.
 XX
 CC This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to CC cDNA clones obtained by an oligo-capping method, where none of these CC clones are identical to any known human mRNAs. The present invention CC describes an immunoassay to identify agonists and antagonists, as well as CC antibodies, antisense molecules and siRNAs that can all be used to bind CC

to and modulate expression of the cDNA molecules. As such, these molecules are useful for diagnostic markers or therapeutic targets for the various diseases or morbid states. In particular, they are useful in gene therapy for treating osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, cytostatic and tranquilliser activities. This polypeptide is a protein encoded by a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but can be obtained on CD-ROM from the European Patent Office, Vienna Sub-office.

XX Sequence 482 AA;

SQ Sequence 482 AA;

Query Match 84.0%; Score 651.5; DB 8; Length 482;

Best Local Similarity 72.0%; Pred. No. 3.4e-56;

Matches 134; Conservative 4; Mismatches 11; Indels 37; Gaps 1;

Qy 1 MKFKLHYNSARQYKDIWNMSDDKPKPELTAPGGCQRFNTNEHDHLA-----43

Db 1 MKFKLHYNSARQYKDLWNMSDDKPKPELTAPGGCQRFNTNEHDHLADQTPTPTRLKNCBEVG 60

Qy 44 -----VHKKHHEMTLKGPARNSKIEBPSVETTHQDSPLPHES 83

Db 61 LFNELASPFENKEPKASEDDIKKMPDLSPLATPIRSKIEBPSVETTHQDSPLPHES 120

Qy 84 TTSDEKEVPLAQTAQPTSAAVRPASLQVNPVLTSSDSSVIIQQAVSPSTSSTVITQAPS 143

Db 121 TTSDEKEVPLAQTAQPTSAAVRPASLQVNPVLTSSDSSVIIQQAVSPSTSSTVITQAPS 180

Qy 144 SNRPIV 149

Db 181 SNRPIV 186

Qy 199 SNRPIV 191

Db 181 SNRPIV 191

RESULT 3

ABB57020

ID ABB57020 standard; protein; 411 AA.

XX AC ABB57020;

XX DT 07-MAR-2002 (first entry)

XX DE Mouse ischaemic condition related protein sequence SEQ ID NO:2.

XX KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;

XX vasospastic ischaemia; ischaemic condition; ischaemic disease.

XX OS Mus musculus.

XX PN WO200188188-A2.

XX PD 22-NOV-2001.

XX PA (UNIV.) UNIV NINHON SCHOOL JURIDICAL PERSON.

XX PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y,

XX DR WPI; 2002-034733/04.

XX N-PSDB; AB19922.

XX 09-DEC-2004.

XX 31-MAY-2004; 2004WO-AU000723.

XX PR 30-MAY-2003; 2003US-0474465P.

XX PA (PHYLOGICA LTD.

XX PI Watt PM, Hopkins R, Bogoyevitch M;

XX DR WPI; 2005-021306/02.

XX 09-DEC-2004.

XX 31-MAY-2004; 2004WO-AU000723.

XX PR 30-MAY-2003; 2003US-0474465P.

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XX 09-DEC-2004.

XX 31-MAY-2004; 2004WO-AU000723.

XX PR 30-MAY-2003; 2003US-0474465P.

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XX PR 30-MAY-2003; 2003US-0474465P.

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XX DR WPI; 2005-021306/02.

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XX 31-MAY-2004; 2004WO-AU000723.

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XX PR 30-MAY-2003; 2003US-0474465P.

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XX DR WPI; 2005-021306/02.

XX 09-DEC-2004.

XX 31-MAY-2004; 2004WO-AU000723.

XX PR 30-MAY-2003; 2003US-0474465P.

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XX PI Watt PM, Hopkins R, Bogoyevitch M;

XX DR WPI; 2005-021306/02.

XX 09-DEC-2004.

XX 31-MAY-2004; 2004WO-AU000723.

XX PR 30-MAY-2003; 2003US-0474465P.

XX PA (PHYLOGICA LTD.

XX PI Watt PM, Hopkins R, Bogoyevitch M;

XX DR WPI; 2005-021306/02.

XX 09-DEC-2004.

XX 31-MAY-2004; 2004WO-AU000723.

XX PR 30-MAY-2003; 2003US-0474465P.

XX PA (PHYLOGICA LTD.

XX PI Watt PM, Hopkins R, Bogoyevitch M;

XX DR WPI; 2005-021306/02.

XX 09-DEC-2004.

XX 31-MAY-2004; 2004WO-AU000723.

XX PR 30-MAY-2003; 2003US-0474465P.

XX PA (PHYLOGICA LTD.

XX PI Watt PM, Hopkins R, Bogoyevitch M;

XX DR WPI; 2005-021306/02.

XX 09-DEC-2004.

XX 31-MAY-2004; 2004WO-AU000723.

XX PR 30-MAY-2003; 2003US-0474465P.

XX PA (PHYLOGICA LTD.

conditions, comprising measuring the expression levels of particular genes in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI99912, encoding the protein sequences in ABB57020 to ABB57274) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic diseases. ABI99913 and ABI99914 represent PCR primers for a mouse ischaemic condition-improving sequence, which are used in the exemplification of the present invention.

XX Sequence 411 AA:
 Qy 57 PARNSKIEPPSVVETTHQDSPLPHPESTISDEKEVPLAQTAQPTSAIVRPAStQVPNTL 116
 Db 23 PIIRSKIEPPSVVETTHQDSPLPHPESTISDEKEVPLAQTAQPTSAIVRPAStQVPNTL 82
 Qy 117 TSSDSSVVIQAVQSPSTSSTVITQAPSNSRPIV 149
 Db 83 TSSSSSVVIQAVQSPSTSSTVITQAPSNSRPIV 115

RESULT 4
 ADP80860 ID ADP80860 standard; protein; 413 AA.
 XX AC ADP80860;

XX DT 09-SEP-2004 (First entry)

XX DE Mouse C130020M04Rik amino acid sequence SEQ ID NO:85.

XX KW c-fos; c-fos interacting protein; fos interacting protein chromosome X;
 KW Fip-cx; screening; fc-fos interacting protein inhibitor; mouse.
 XX OS Mus musculus.
 PN WO2004053121-A1.
 XX 24-JUN-2004 .
 PD XX PR 19-NOV-2003; 2003WO-JP014749.
 XX PR 11-DEC-2002; 2002JP-00360046.
 XX PA (UYKE-) UNIV KEIO.

XX PT New Proteins that interact with fos, e.g., fos interacting protein
 PT Chromosome X (Fip-cx).
 XX DR 2004-517250/49.
 PS N-PSDB; ADP80924.

XX Claim 57; SEQ ID NO 85; 192PP; Japanese.

XX The present invention describes a protein (I) that interacts with c-fos (e.g., fos interacting protein chromosome X (Fip-cx), Fip-cx.1, fos interacting protein chromosome ex.2, or fos interacting protein chromosome 4). Also described: (1) a nucleic acid (II) that encodes (I); (2) an inhibitor (III) that inhibits the interaction of (I) encoded by (II) with c-fos protein; (3) an inhibitor (IV) that inhibits interaction of a protein as mentioned in (3) with c-fos protein; and (4) detecting (M1) the interaction of a protein as mentioned in (3) with c-fos protein by contacting the protein with c-fos, to form a composite. (I) is useful for detecting its interaction with c-fos, to form a complex. (M1) is useful for screening the protein that interacts with c-fos which involves performing the detection process and selecting the protein that interacts with c-fos which (M1) is useful for screening a protein that interacts with c-fos which involves performing the detection of the detected protein. (I) is useful for screening inhibitors that interact with c-fos. The present sequence represents a mouse C130020M04Rik amino acid sequence, which can interact with c-fos in the exemplification of the present invention.

XX SQ Sequence 413 AA:
 Qy 19 MSDDKPKFLCTAPCGQRTPTNEDHLAVKHKHENTLKGCPARISKI-----63
 Db 1 MGDDRPFVCSAPCGQRTPTNEDHLAVKHKHENTLKGSPARTDSVIALADQTPPTPTRLKN 60
 Qy 64 -----EEPSVYETTHOD 75
 Db 61 CBEVGLNFELASSFEHEKKAKSDDDEKKGAAGLDMSLIPSTDKIKEEPEVSDSSPPD 120
 Qy 76 SPLPHPESTISDEKEV---PLAQTAAQPTSAIVRPAStQVPNTLTSDDSVI1QQAVPSP 132
 Db 121 SPASSPCSPPLKEKEVTTKPVV-1STPPTIVRPGSLP---LHLGTD---LHPTLSP 172
 Qy 133 TSSTVITQAPSNSRPI 148
 Db 173 TS--VITQAPSNSRQI 186

RESULT 5
 ADC18733 ID ADC18733 standard; protein; 501 AA.
 XX AC ADC18733;
 XX DT 18-DEC-2003 (first entry)
 XX DE Human cyclic AMP response-element binding protein, CREBPA.
 XX KW candidate cell death pathway modulating agent; CREBPA; cytosstatic;
 KW cyclic AMP response-element binding protein; CREBPA; cancer; human; gene;
 KW angiogenic; apoptotic; cell proliferation disorder; cancer; human; gene;
 KW ds.
 XX OS Homo sapiens.
 XX PN WO2003074672-A2.
 XX PD 12-SEP-2003.
 XX AX PR 01-MAR-2002; 2002US-0360810P.
 XX PR 01-MAR-2002; 2002US-0360810P.
 XX PA (EXEL-) EXELIXIS INC.
 XX PI Costa MA, Parry D, Chen C,
 XX DR WPI; 2003-71288/67.
 XX N-PSDB; ADC18732.

XX Identifying candidate cell death pathway modulators for treating cell death-related diseases, comprises contacting an assay system comprising cyclic AMP response-element binding protein, and detecting test agent biased activity.
 XX Example I; SEQ ID NO 2; 49PP; English.

XX The invention relates to a novel method for identifying a candidate cell death pathway modulating agent. The novel method comprises contacting an

assay system comprising a cyclic AMP response-element binding protein (CREBPA) polypeptide or a nucleic acid, with a test agent, and detecting a test agent-biased activity of the assay system. Identifying a candidate cell death pathway modulating agent comprises providing an assay system comprising a CREBPA polypeptide or a nucleic acid; contacting the assay system with a test agent under conditions, where in the presence of the test agent, the system provides a reference activity, and detecting a test agent-biased activity of the assay system, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate cell death pathway modulating agent. The candidate cell death pathway modulating agents have cytostatic activity. The method is useful for identifying candidate cell death pathway modulating agents, which may be used as candidate therapeutic agents for treating disorders associated with defective or impaired cell death and/or CREBPA function, such as angiogenic; apoptotic or cell proliferation disorders, e.g. cancer. Nucleic acid modulators may be used as research reagents, diagnostics, and therapeutics for treatment of cell death-related disease states. This sequence represents the human CREBPA protein of the invention.

Sequence 501 AA:

```
Query Match 33.6%; Score 260.5; DB 7; Length 501;
Best Local Similarity 37.8%; Pred. No. 4.3e-17;
Matches 59; Conservative 21; Mismatches 41; Indels 35; Gaps 3;
```

```
Qy 18 NMSDDKPKPLCTAPGCCQRFETNEDHLAVHKHKGHEMTLKFGRDARNSKLEEPVETTHQDSP 77
Db 2 NLEQERPSVCSAPGCSQRFTEDHLIMTHRKGHEMTLKF-----PAIKTDMMLSDQ 51
Qy 78 LPHP-----ESTSDEKEVPLAQTAOPT-----SAIVRPAASLQVP 112
Db 52 TPTPPTPRLKNGEEVGLFSEELQSCSLERFRKQQESESSKRNTSMNAVGGMGTPOTHQLS 111
Qy 113 NYVLTSSDSVYLQQAVPSPTSPSTSSTVITQAPSNSNRPI 148
Db 112 SARLPNHDNTVVIQQAMPSPQSSSVITQAPSNTRQI 147
```

RESULT 6
 ID AAG02942 standard; protein; 52 AA.
 AC AAG02942;
 XX DT 06-Oct-2000 (first entry)
 DE Human secreted protein, SEQ ID NO: 7023.
 XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
 XX Homo sapiens.
 XX PN EP1033401-A2.
 XX PD 06-SEP-2000.
 XX PF 21-FEB-2000; 2000EP-00200610.
 XX PR 26-FEB-1999; 99US-0122487P.
 XX PA (GEST) GENSET.
 XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX P1 2000-500381/45.
 DR N-PSDB; AAC02948.
 XX New nucleic acid that is a 5' expressed sequence tag ('EST') for obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.

Claim 13; SEQ ID NO 7023; 71PP + Sequence Listing; English.
 XX The present sequence is a polypeptide encoded by one of a large number of CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were CC prepared from total human RNAs or polyA+ RNAs derived from 30 different CC tissues. EST sequences usually correspond mainly to the 3' untranslated CC region (UTR) of the mRNA because they are often obtained from oligo-dT CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA CC sequences derived from the 5' ends of mRNAs and even in those cases where CC longer cDNA sequences have been obtained, the full 5' UTR is rarely CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs CC are also used in diagnostic, forensic, gene therapy and chromosome CC mapping procedures. They are used to obtain upstream regulatory sequences CC and to design expression and secretion vectors.
 XX SQ Sequence 52 AA;

Query Match	Score	DB	Length
Best Local Similarity	27.3%	3	52;
Matches	Pred. No. 1.5e-13;	3; Mismatches	Indel 8
Conservative	36;	6;	0; Gaps 0;

Qy 19 MSDDKPKPLCTAPGCCQRFETNEDHLAVHKHKGHEMTLKFGRDARNSKI 63
 Db 1 MGDDDRXPFVNAPGCCQRFETNEDHLAVHKHKGHEMTLKFGRDARTDSV 45

RESULT 7
 ID AAB68325 standard; peptide; 29 AA.
 XX AC AAB68325;

Qy 20 RRIKTDMLSDQ 51
 Db 20 AAB68325

DE c-Jun amino terminal kinase (JNK) inhibitor Peptide ATF2.

XX DT 09-JUL-2001 (first entry)

XX KW c-Jun amino terminal kinase; JNK; retenosis; oncogenic transformation; immune cell; proinflammatory cytokine; ionizing radiation; ischemia; reperfusion; hypoxia; hyperthermia; apoptosis; diabetes; cardiovascular disease; myopathy; cardiomyopathy; graft rejection; degenerative disease; hypertension; arterial occlusive lesion; arteriosclerotic lesion; hypothermia; cell proliferative disease; psoriasis; pemphigus vulgaris; Behcet's syndrome; acute respiratory distress syndrome; leukemia; rheumatoid arthritis; AIDS; vasculitis; septic shock; lipid histocytosis. KW Synthetic.

OS WO200127268-A2.

XX PD 19-APR-2001.

XX PF 12-OCT-2000; 2000WO-1B001538.

XX PR 12-OCT-1999; 99US-0158774P.

PR 14-FEB-2000; 2000US-00503954.

XX PA (UCLA-) UNIV LAUSANNE.

XX PI Bonny C;

XX DR WPI, 2001-308260/32.

XX PT New Peptide inhibitors of the c-Jun amino terminal kinase (JNK) pathway PT useful for treating inflammatory, immune or degenerative disorders e.g. AIDS, leukemia, graft rejection, diabetes, rheumatoid arthritis, ischemia.

XX PS Claim 31; Page 6; 51PP; English.

XX PT AAB63306-25 represent peptides which inhibit c-Jun amino terminal kinase CC (JNK). The peptides are used to alter a JNK effect when present in a JNK- CC

expressing cell, where the effect is restenosis, oncogenic transformation, maturation and differentiation of immune cells, proteinflammatory cytokines, ionizing radiation as used in radiotherapy, ultraviolet light, free radicals, DNA damaging agents, chemotherapeutic drugs, ischemia, reperfusion, hypoxia, hypotension, apoptosis, response to stressful stimuli, diabetes and heart/cardiovascular hypertrophy. They can also be used to treat inflammatory, autoimmune, immune, autoimmune, degenerative diseases, myopathies, cardiomopathies and graft rejection and to treat or prevent arterial hypertension, cardiac hypertrophy, arteriosclerotic lesions and hypertension. The JNK inhibitor peptides are also useful in treating non-malignant or immunological related cell proliferative diseases such as psoriasis, pemphigus vulgaris, Benet's syndrome, acute respiratory distress syndrome, leukemia, rheumatoid arthritis, AIDS, vasculitis, septic shock and lipid histocytosis.

Sequence 29 AA;

Query Match Score 137; DB 4; Length 29;
Best Local Similarity 88.9%; Pred. No. 2.2e-06;
Matches 24; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 37 TNEDHLAVHKHKGHENLTKFGPARNISKI 63
Db 1 TNEDHLAVHKHKGHENLTKFGPARNDSV 27

RESULT 8
ID ADF17925

standard; peptide; 29 AA.

XX
XX
AC
XX
DT 12-FEB-2004 (first entry)

Synthetic JNK inhibitor peptide ATF2 used to treat hearing loss.
JNK inhibitor peptide; hearing loss; c-Jun amino terminal kinase; JNK; noise trauma; antibiotic treatment; chemotherapeutic agent; pancreatic islet cell death; diabetes; autoimmune disease; cardiovascular; cancer; immunosuppressive; auditory; antidiabetic; immunosuppressive; cardiant; cytostatic; neuronal apoptosis; hair cell stereocilia.
Synthetic.
XX
PN US2003100539-A1.
XX
PD 12-JUN-2003.
XX
PF 07-JUN-2002; 2002US-00165250.
XX
PR 14-FEB-2000; 2000US-00503954.
PR 09-JAN-2002; 2002US-0347052P.
XX
(BONN/) BONNY C.
PA
PI
DR
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PT
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PR
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PA
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PI
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DR
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PS

Preventing or treating hearing loss in a subject, by administering a cell -permeable bioactive peptide, which prevents damage to the hair cell stereocilia, hair cell apoptosis or neuronal apoptosis.

Example 1: SEQ ID NO 20; 39pp; English.

This invention relates to a novel method for preventing or treating hearing loss in a subject. Specifically, it comprises administering a cell-permeable bioactive peptide, which inhibits the activated c-Jun amino terminal kinase (JNK) signalling pathway. This pathway is implicated in the control of cell growth and differentiation, and is activated in response to environmental stimuli. Accordingly, the present

invention describes administration of a bioactive peptide that prevents damage to the hair cell stereocilia, hair cell apoptosis or neuronal apoptosis caused by either noise trauma, antibiotic treatment (e.g. amineglycoside) or a chemotherapeutic agent. Furthermore, these peptides can be useful for inhibiting pancreatic islet cell death, as well as for treating diabetes, autoimmune disease, cardiovascular disease and some cancers. As such, they can be described as immunosuppressive, auditory, antidiabetic, immunosuppressive, cardiant and cytostatic. This peptide sequence is the JNK inhibitor peptide of the invention.

Sequence 29 AA;

Query Match Score 137; DB 7; Length 29;
Best Local Similarity 88.9%; Pred. No. 2.2e-06;
Matches 24; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 37 TNEDHLAVHKHKGHENLTKFGPARNISKI 63
Db 1 TNEDHLAVHKHKGHENLTKFGPARNDSV 27

RESULT 9

ID AD001349

standard; peptide; 29 AA.

XX
AC
XX
XX
DT 15-JUL-2004 (first entry)
XX
DE c-Jun amino terminal kinase; JNK; signal transduction pathway;
XX
KW c-Jun amino terminal kinase; JNK; signal transduction pathway;
KW neuronal cell damage; ischemic injury; reperfusion injury;
KW neuronal disorder; stroke; amyotrophic lateral sclerosis; epilepsy;
KW multiple sclerosis; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; neurodegenerative disease;
KW human immunodeficiency virus dementia; inhibitor; therapy.
Unidentified.

OS US2004082509-A1.
XX
XX
PD 29-APR-2004.
XX
XX
PF 09-JUN-2003; 2003US-00457614.
XX
PR 12-OCT-1999; 93US-015871P.
PR 14-FEB-2000; 2000US-00503934.
PR 09-JAN-2002; 2002US-0347052P.
PR 07-JUN-2002; 2002US-00165250.
XX
(BONN/) BONNY C.
PA
PI
DR
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PT
XX
PT
XX
PT
XX
PS

Example 1: SEQ ID NO 20; 54PP; English.

The invention relates to cell-permeable peptide inhibitors of the c-Jun amino terminal kinase (JNK) signal transduction pathway. The cell-permeable peptides are useful for inhibiting neuronal cell damage, ischemic or reperfusion injury, neuronal cell death in a subject or treating a neuronal disorder. The neuronal disorder is selected from stroke, amyotrophic lateral sclerosis, epilepsy, multiple sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, neurodegenerative disease, and human immunodeficiency virus dementia. The present sequence is a JNK inhibitor peptide.

Example 1: SEQ ID NO 20; 54PP; English.

The invention relates to cell-permeable peptide inhibitors of the c-Jun amino terminal kinase (JNK) signal transduction pathway. The cell-permeable peptides are useful for inhibiting neuronal cell damage, ischemic or reperfusion injury, neuronal cell death in a subject or treating a neuronal disorder. The neuronal disorder is selected from stroke, amyotrophic lateral sclerosis, epilepsy, multiple sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, neurodegenerative disease, and human immunodeficiency virus dementia. The present sequence is a JNK inhibitor peptide.

xx	SQ	Sequence 29 AA;	Query Match Score 137; DB 8; Length 29;	xx	Db	823 LTI 825
Best Local Similarity 88.9%; Pred. No. 2.2e-06;						
Matches 24; Conservative 1; Mismatches 2; Indels 0; Gaps 0;						
RESULT 11						
AAE18363						
ID AAE18363 standard; protein: 364 AA.						
XX						
XX						
KW BVH-P1 gene; streptococcal infection; pharyngitis; erysipelas; impetigo;						
KW scarlet fever; bacteraemia; necrotising fascitis; toxic shock; vaccine;						
KW immune response; anti-inflammatory; immunisation; antibacterial.						
XX						
XX Streptococcus pyogenes strain SP57 BVH-P1 mature protein.						
DE DE						
XX XX						
KW BVH-P1 gene; streptococcal infection; pharyngitis; erysipelas; impetigo;						
KW scarlet fever; bacteraemia; necrotising fascitis; toxic shock; vaccine;						
KW immune response; anti-inflammatory; immunisation; antibacterial.						
XX						
XX Streptococcus pyogenes, SP57.						
OS OS						
XX XX						
XX Streptococcus pyogenes strain SP57 BVH-P1 mature protein.						
WO200204495-A2.						
PD 07-OCT-2004 (First entry)						
XX XX						
DE Mouse cancer associated sequence MP2-08-013, SEQ ID 182.						
XX XX						
KW Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Mouse.						
OS OS						
XX Mus musculus.						
XX XX						
XX WO2004060304-A2.						
XX XX						
PD 22-DEC-2003; 2003WO-US041389.						
XX XX						
PF 22-DEC-2002; 2002US-00330773.						
XX XX						
(SAGR-) SAGRES DISCOVERY INC.						
PA PA						
PI Morris DW, Malandro MS;						
PT DR; 2004-543781/52.						
XX XX						
PT New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.						
PT XX						
PT PS Claim 1; SEQ ID NO 182; 199pp; English.						
PT XX						
CC The present invention relates to cancer associated sequences (ADQ97025-CC 04). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format directly from WIPO at CC ftp://wipo.int/pub/published_pct_sequences.						
CC XX						
CC Sequence 1483 AA;						
PT Query Match Score 110.5; DB 8; Length 1483;						
PT Best Local Similarity 26.2%; Pred. No. 0.17;						
PT Matches 48; Conservative 22; Mismatches 64; Indels 49; Gaps 9;						
CC SQ Sequence 364 AA;						
CC SQ Query Match Score 109; DB 5; Length 364;						
CC Best Local Similarity 28.5%; Pred. No. 0.036;						
CC Matches 35; Conservative 22; Mismatches 36; Indels 30; Gaps 5;						
CC SQ Updated on 29-AUG-2003 to standardise OS field						
Qy 9 SARQYKD--LWAMS-DDKPKFLCTAPGCGQRFNED---HLAVKH-----KH 49						
Qy 649 SATNYKHYRHTVSPGEKPYCTVPGCKRFTEYSSLYKHHVHTHCKPYTCSSCGKTY 708						
Db 50 EMTLKFGPARNSKIEEPVSVETHQ-----DSPLPHPB-----STSDEKEVP 92						
Db 709 RQFSTLNRHSANGELATEESEQALYEQQQLEAASARESPPKPHTAYLSERVE - 766						
Db 93 LAQTAQPTSAIVPASLQVNPYLTLTSDSSVIIQQAVPS-----TSSTVITOAPSNN 145						
Db 767 -ESSAQTQVAMTYEEDEGPQVQUALITQD---QVSVSLSPEDIOLQGSAISVYQHGTSIT 822						
Db 146 RPI 148						

Db	192	RPV 194	Qy	108 SLQVPNVILTSSDSSV-----IIQQAVSPSTSS-----TVITQAP-SSN 145
ABP25889			Db	157 SSVTASSELTSSTRVVSTELSESQKQPVEVTPKAERTTEVPEPKTDISEAITSAN 216
ID ABP25889	standard; protein;	389 AA.	Qy	146 RPI 14.8
XX			Db	217 RPV 219
AC ABP25889;				
XX	02-JUL-2002	(First entry)	RESULT 13	
DE Streptococcus polypeptide SEQ ID NO 954.			AAE18359	standard; protein; 389 AA.
XX	KW GBS: group B streptococcus; Streptococcus agalactiae;		ID AAE18359	
KW group A streptococcus; Streptococcus pyogenes; antibacterial;			XX	
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.			AC AAB18359;	
XX	Streptococcus pyogenes.		XX	
OS WO200234771-A2.			DT 29-AUG-2003 (revised)	
PN XX	BVH-P1 gene; streptococcal infection; pharyngitis; erysipelas; impetigo;		DT 07-MAY-2002 (first entry)	
PD 02-MAY-2002.	KW scarlet fever; bacteraemia; necrotising fascitis; toxic shock; vaccine;		XX	
XX immune response; anti-inflammatory; immunisation; antibacterial.			DE Streptococcus pyogenes strain SPY57 BVH-P1 protein.	
PP 29-OCT-2001; 2001WO-GB004789.			XX	
PR 27-OCT-2000; 2000GB-00026333.			Key Location/Qualifiers	
PR 24-NOV-2000; 2000GB-00028727.			1; 25	
PR 07-MAR-2001; 2001GB-00005640.			label= signal_peptide	
XX (CHIR-) CHIRON SPA.			26 .389	
PA (GENO-) INST GENOMIC RES.			/note= "Mature_BVH_P1_protein"	
XX WO200204495-A2.			XX	
PI Telford J, Mabignani V, Margarit Y Rossi, Grandi G, Frazer C;			PN WO200204495-A2.	
PI Tettelin H;			XX	
XX DR 2002-352516/38.			PD 17-JAN-2002.	
DR N-PSDB; ABN66520.			XX	
XX PT New Streptococcus protein for the treatment or prevention of infection or			PF 06-JUL-2001; 2001WO-CA001001.	
PT disease caused by Streptococcus bacteria, such as meningitis, and for			PR 06-TUL-2000; 2000US-0216465P.	
PT detecting a compound that binds to the protein.			XX (SHIR-) SHIRE BIOCHEM INC.	
XX Claim 1; Page 3249; 4525pp; English.			PI Martin D, Hamel J, Brodeur B;	
PS The invention relates to a protein (ABP25413:ABP0895) from group B			XX WPI; 2002-171701/22.	
XX streptococcus bacteria, particularly S. agalactiae and S. pyogenes.			DR N-PSDB; AAD2994.	
CC Nucleic acids encoding (I) are used to detect Streptococcus/GAS			XX	
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1). Given			CC The invention relates to antigens, more particularly an antigen of	
CC the specification. The proteins have antibacterial and antiinflammatory			CC Streptococcus pyogenes (also called group A Streptococcus (GAS))	
CC activity (I), nucleic acids encoding (I), ABN6644-ABN71546 and			CC bacterial pathogens. The polypeptides and polynucleotides encoding them	
CC antibodies that bind (I) are used in the manufacture of medicaments for			CC are useful for diagnosing, preventing or treating streptococcal	
CC the treatment or prevention of infection or disease caused by			CC infection, such as pharyngitis, erysipelas, impetigo, scarlet fever,	
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.			CC invasive diseases (bacteræmia, necrotising fascitis, toxic shock), and	
CC Nucleic acids encoding (I) are used to determine whether a compound binds to			CC for eliciting an immune response. The polypeptides may also be used as	
CC a biological sample. (I) is used to determine whether a compound binds to			CC immunogens for producing antibodies for the diagnosis and treatment of	
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be			CC Streptococcus infection, for passive immunisation. DNAs encoding	
CC used as a vaccine or diagnostic composition. The disease caused by			CC polypeptides may also be used to design DNA probes for detecting the	
CC Streptococcus that is prevented or treated may be meningitis. Nucleic			CC presence of Streptococcus in biological samples suspected of containing	
CC acid encoding (I) may be used to recombinantly produce (I) and may be			CC the bacteria. The vaccine composition is useful as a prophylactic or	
CC used in gene therapy. Antibodies to (I) are used for affinity			CC therapeutic treatment of Streptococcal infection in an individual	
CC chromatography, immunoassays, and distinguishing/identifying			CC susceptible to or infected with streptococcal infection. The present	
CC Streptococcus proteins			CC sequence is Streptococcus pyogenes strain SPY57 BVH-P1 protein. (Updated	
XX Sequence 389 AA;			on 29-AUG-2003 to standardise OS field)	
Query Match 14.0%; Score 109; DB 5; Length 389;			XX	
Best Local Similarity 28.5%; Pred. No. 0.042;			SQ Sequence 389 AA;	
Matches 35; Conservative 22; Mismatches 36; Indels 30; Gaps 5;			Query Match 14.0%; Score 109; DB 5; Length 389;	
Qy 56 GPARNISKIEP-SVYETTHODSPLPHEPESTSDEKEVPLAQTAQTS-----AVRA 107				
Db 97 QGATNLTVQAPASSPASVSVAVPSSEPLPQASATSPVMPAPPSPDVTPFPPASA 156				

Qy 2 KPKLAVNSARQYKDLWNMSDDKPFCLCTAPGCQQRFTNEDHLAVHKHHEMTLKFGD---- 57
286 KYKL-VNHIRVH-----TGERKPFPCPFPGCKVFARESNKIHCRTHGKPFKEFFG 338
Db 58 -----ARNSKIBEPSSVYETHQ-----DSPLPHPESTSDEK-EVPLAQTAAOPTSAIV 104
Qy 339 CDRRFANSSDRKXHMAVHTSDKPYLCKMCDSYTHSSVRKHMVKHESSSQGSQPSA-- 396
Db 105 RPASLQVYPNVLTSSDVVIQQAVPBSPTTSSTVITQAPSNN 145
Qy 397 -----ASGYBSSTPPPTIVSPSTDNPNTSSL---SPSSS 427

Search completed: January 10, 2006, 23:05:08
Job time : 138 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	736	94.8	505	1 S05380	transcription fact activating transcr cyclic AMP respons CAMP response elem CAMP respons elem transcription fact CAMP respons elem cyclic AMP respons zinc finger protein zinc Protein - mouse zinc finger protein hypofingerl zinc odd paired fruit developmental cont glucan 1,4-alpha-g carbon catabolite zinc finger protein - neural specific DN metal-responsive t protein C27A12.3 [transcription fact finger protein - zinc finger protein GT box-binding pro zinc finger protein - spalt Protein - mo DNA binding protei finger protein odd
2	594	76.5	486	2 JG4028	
3	450	58.0	456	2 BA2026	
4	445	57.3	448	2 A42026	
5	363	46.8	389	1 A39429	
6	295	38.0	483	2 S12741	
7	260.5	33.6	508	1 A45477	
8	180	23.2	358	2 C42026	
9	170	21.9	313	2 A34785	
10	113	14.6	428	2 T43532	
11	107	13.8	447	2 J56511	
12	107	13.8	515	2 A44256	
13	107	13.0	582	2 T38743	
14	103	13.3	609	2 A49839	
15	102.5	13.2	533	2 M020304	
16	102.5	13.2	1367	1 S48478	
17	102	13.1	409	2 S10704	
18	102	13.1	565	2 T39863	
19	100.5	13.0	1361	2 T30884	
20	99.5	12.8	593	2 UC7829	
21	98	12.6	532	2 BC7793	
22	97.5	12.6	696	2 A29635	
23	97	12.5	1402	2 S42748	
24	95	12.2	353	2 BC4875	
25	95	12.2	697	2 BC4489	
26	95	12.2	1350	2 T30341	
27	94.5	12.2	1323	2 T120253	
28	94.5	12.2	1360	2 T12064	
29	94	12.1	392	2 S11998	

RESULT 1									
S05380									
transcription factor ATP2 - human									
N;Alternate names: activating transcription factor 2 (ATP-2); cAMP response element-binder									
N;Contains: cAMP response element-binding protein HB16									
C;Species: Homo sapiens (man)									
C;Date: 10-Sep-1999 #Sequence_revision 10-Sep-1999 #text_change 09-Jul-2004									
C;Accession: S05380; A34776; B34223									
R;Mieka, T.; Sakura, H.; Kanai-Ishii, C.; Sudo, T.; Fujisawa, J.I.; Yo									
EMBO J. 6, 2033-2038, 1989									
A;Title: Leucine zipper structure of the protein CRE-BP1 binding to the cyclic AMP resp									
A;Reference number: S05380; MUID:90005408; PMID:9029117									
A;Accession: S05380									
A;Molecule type: mRNA									
A;Residues: 1-505 <M4>									
A;Cross-references: UNIPARC:UPI00016AA16; GB:M31630; PID:9183787; PDB:AAA35951.1; PID:R;Kara, C.J.; Liou, H.C.; Ivashkin, L.B.; Gimicher, L.H.									
R;Liu, T.; Liu, F.; Coukos, W.J.; Green, M.R.									
Mol. Cell. Biol. 10, 1347-1357, 1990									
A;Title: A cDNA for a human cyclic AMP response element-binding protein which is distin									
A;Reference number: A34776									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 211-222, 'N', 224-505 <SKAR>									
A;Cross-references: UNIPARC:UPI00016AA16; GB:M31630; PID:9183787; PDB:AAA35951.1; PID:R;Huang, Y.; Liu, F.; Coulouarn, E.; Green, M.R.									
Genes Dev. 3, 2083-2090, 1989									
A;Title: Transcription factor ATF cDNA clones: an extensive family of leucine zipper pr									
A;Reference number: A91622; MUID:90185187; PMID:2516827									
A;Status: nucleic acid sequence not shown; not compared with conceptual translation									
A;Molecule type: mRNA									
A;Residues: 1-505 <HA2>									
A;Cross-references: UNIPARC:UPI0001748C4									
C;Genetics:									
A;Gene: GDB:ATF2; CREB2; TREB7; CRE-BP1									
A;Cross-references: GDB:128011; OMIM:123811									
A;Residues: 107-357, 'V', 359-465 <HA2>									
A;Cross-references: UNIPARC:UPI0001748C4									
C;Superfamily: cAMP response element-binding protein 1; fos/jun DNA-binding domain homology <FJD>									
F;347-387/Domain: fos/jun DNA-binding domain homology									
Query Match 94.8% Score 736; DB 1; Length 505;									
Best Local Similarity 71.3%; Pred. No. 7.9e-55; Mismatches 0; Indels 60; Gaps 1;									
Matches 149; Conservative 291-2912									
C;Keywords: alternative splicing; DNA binding; nucleus; transcription regulation									
Qy 1 MKPKLHNNSARQYDLMWNSDDDKPFLCTAPGGCQRTNEDHLAVHKHKBMTLKGFPARN 60									
Db 1 MKPKLHNNSARQYDLMWNSDDDKPFLCTAPGGCQRTNEDHLAVHKHKBMTLKGFPARN 60									
Qy 61 -----									

ALIGNMENTS

Total number of hits satisfying chosen parameters: 283416

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		C; Superfamily: cAMP response element-binding protein 1; fos/jun DNA-binding domain homolog <FJD>
Db	61 DSVIVADQPTPTEFLKNCIEEVGLFNELASPFENEFFKASEDDIKMPMLDLSPATPIIR 120	F; 297-337; Domain: fos/jun DNA-binding domain homology <FJD>
Qy	61 SKIEEPSSVETTHQDSPLPHPESTTSDEKEVPLAQTAAQPTSAIVRASLQOPENVNLTLSSD 120	Query Match Score 58.0%; Best Local Similarity 67.3%; Matches 99; Conservative 0; Mismatches 0; Indels 60; Gaps 1;
Db	121 SKIEEPSSVETTHQDSPLPHPESTTSDEKEVPLAQTAAQPTSAIVRASLQOPENVNLTLSSD 180	Qy 51 MTLKEFGPARN-----
Qy	121 SSVIQQAVAPSPTSSTTVITQAQSSNRPIV 149	Db 1 MTLKEFGPARNDSVIVADQPTPTEFLKNCIEEVGLFNELASPFENEFFKASEDDIKMPMLD 60
Db	181 SSVIQQAVAPSPTSSTTVITQAQSSNRPIV 209	Qy 61 -----SKIEEPSSVETTHQDSPLPHPESTSDEKEVPLAQTAAQPTSAIVRASLQ 110
RESULT 2		
JC4028	activating transcription factor 2 - African clawed frog	Db 61 LSPLATPIIRSKIEEPSSVETTHQDSPLPHPESTSDEKEVPLAQTAAQPTSAIVRASLQ 120
C; Species: Xenopus laevis (African clawed frog)	C; Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004	Qy 111 VPNVLTTSQPSVVIQQAQVPSPTSSTVTOAPSSNRPIV 149
C; Accession: JC4028	P; Villarreal, X.C.; Richter, J.D.	Db 121 VPNVLTTSQSSVVIQQAQVPSPTSSTVTOAPSSNRPIV 159
Gene 153 225-229, 1995	A; Title: Analysis of AP2 gene expression during early Xenopus development nt.	RESULT 4
A; Reference number: JC4028; MUID:95180723; PMID:7875593	A; Accession: JC4028	A42026
A; Molecule type: mRNA	A; Molecule type: mRNA	Camp response element-binding protein 3 - mouse
A; Residues: 1-486 <VIL>	A; Residues: 1-486 <VIL>	C; Species: Mus musculus (house mouse)
A; Cross-references: UNIPROT:Q91576; UNIPARC:UPI00000FB2FD; GB:U16158; NID:9887779; PIDN: C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999	A; Note: sequence extracted from NCBI backbone (NCBIN:76655, NCBI:76616)	C; Accession: A42026
A; Comment: This protein is a sequence-specific DNA-binding protein that mediates transcriptional regulation by binding to AP2 sites in target genes.	R; Georgopoulos, K.; Morgan, B.A.; Moore, D.D.	R; Georgopoulos, K.; Morgan, B.A.; Moore, D.D.
C; Superfamily: cAMP response element-binding protein 1; fos/jun DNA-binding domain homolog	C; Superfamily: cAMP response element-binding protein 1; fos/jun DNA-binding domain homolog	Mol. Cell. Biol. 12, 747-757. 1992
C; Keywords: leucine zipper; phosphoprotein; transcription regulation	A; Title: Functionally distinct isoforms of the CRE-BP DNA-binding protein mediate activation of the AP-2 promoter. A; Reference number: A42026; MUID:92123199; PMID:1531087	A; Content: El4
P; 329-369; Domain: fos/jun DNA-binding domain homology <FJD>	P; 329-364; Region: basic	A; Status: preliminary
P; 82/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted	P; 82/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted	A; Molecule type: mRNA
P; 102/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted	P; 102/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted	A; Residue: 1-48 <GEO>
Query Match Score 594; DB 2; Length 486;	Query Match Score 594; DB 2; Length 486;	A; Cross-references: UNIPARC:UPI0000170CB5; GB:876555; NID:9243426; PIDN: AAB21127.1; PIDN: 76616
Best Local Similarity 64.9%; Pred. No. 86-43; Indels 3; Gaps 2;	Best Local Similarity 64.9%; Pred. No. 86-43; Indels 3; Gaps 2;	A; Note: sequence extracted from NCBI backbone (NCBIN:76655, NCBI:76616)
Matches 124; Conservative 4; Mismatches 4;	Matches 124; Conservative 4; Mismatches 4;	C; Superfamily: camp response element-binding protein 1; fos/jun DNA-binding domain homology <FJD>
Qy 19 MSDDKPKFLCTAPCGQFRFTNEHDHLAVHKHKGEMTLLKEGPARN----- 60	Qy 17 WNMSSDKP-----FL-CTAPG----CGQFRFTNEHDHLAVHKHKGEMTLLKEGPAR----NSK 62	Matches 103; Conservative 1; Mismatches 1; Indels 18; Gaps 4;
Db 1 MSDDKPKFLCTAPCGQFRFTNEHDHLAVHKHKGEMTLLKEGPARNDSVIVADQPTPTEFLKN 60	Db 5 WWPDPQTPTPTEFLKNCIEEVGLFNELASPFENEFFKASEDDIKMPMLDLSPLATPIIRSK 64	Query Match Score 445; DB 2; Length 448;
Qy 61 -----SKIEEPSSVETTHQDSPLP 79	Qy 63 IEEPSVETTHQDSPLPHPESTSDEKEVPLAQTAAQPTSAIVRASLQOPENVNLTSQDSS 122	Best Local Similarity 70.1%; Pred. No. 3e-30; Indels 29; Gaps 14;
Db 61 CEEVGLFNELASPFENEFFKASEDDIKMPMLDLSPLATPIIRSKIEEPSSVETTHQDSPLP 120	Db 65 IEEPSVETTHQDSPLPHPESTSDEKEVPLAQTAAQPTSAIVRASLQOPENVNLTSQDSS 124	Matches 103; Conservative 1; Mismatches 1; Indels 18; Gaps 4;
Qy 80 HPESTTSDE-KEYPLAQTAAQPTSAIVRASLQOPENVNLTSQDSSVVIQQAQVPSPTSTVI 138	Qy 123 VIQQQAVPSPTSSTVTOAPSSNRPIV 149	Query Match Score 57.3%; Best Local Similarity 70.1%; Pred. No. 3e-30; Indels 29; Gaps 14;
Db 121 HPESTTSQHNQVPLAQTAQPTSAIVRASLQOPENVNLTSQDSSVVIQQAQVPSPTSTVI 180	Db 125 VIQQQAVPSPTSSTVTOAPSSNRPIV 151	Matches 103; Conservative 1; Mismatches 1; Indels 18; Gaps 4;
Qy 139 TOAPSSNRPIV 149		Qy 123 VIQQQAVPSPTSSTVTOAPSSNRPIV 149
Db 181 TQAPSTNSIV 191		Db 125 VIQQQAVPSPTSSTVTOAPSSNRPIV 151
RESULT 3		
B42026	cyclic AMP response element DNA-binding protein 1 - mouse	A39429
C; Species: Mus musculus (house mouse)	C; Species: Rattus norvegicus (Norway rat)	Camp response element-binding protein ATP2 - rat
C; Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999	C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004	C; Accession: A39429
R; Georgopoulos, K.; Morgan, B.A.; Moore, D.D.	R; Kageyama, R.; Sasai, Y.; Nakaniishi, S.	C; Accession: A39429
Mol. Cell. Biol. 12, 747-757. 1992	J. Biol. Chem. 266, 15525-15531. 1991	A; Title: Molecular characterization of transcription factors that bind to the cAMP resp
A; Title: Functionally distinct isoforms of the CRE-BP DNA-binding protein mediate activation of the AP-2 promoter. A; Reference number: A42026; MUID:92123199; PMID:1531087	A; Content: El4	A; Reference number: A39429; MUID:9133205; PMID:1714459
A; Accession: B42026	A; Status: preliminary	A; Accession: A39429
A; Molecule type: mRNA	A; Molecule type: mRNA	A; Status: preliminary
A; Residues: 1-456 <GEO>	A; Residues: 1-369 <GEO>	A; Molecule type: mRNA
A; Cross-references: UNIPARC:UPI0000170CB6; GB:876657; NID:9243428; PIDN:AAB21128.1; PIDN: 76657; NCBI:76657	A; Cross-references: UNIPROT:Q00969; UNIPARC:UPI000002A474; GB:ME65148; NID:9206569; PIDN: 76657; NCBI:76657	C; Superfamily: camp response element-binding protein 1; fos/jun DNA-binding domain homolog

Db	107	: vPSV-----PGIPGSS 118	Qy	145 NR 146 :
RESULT 9				
A34785	DNA-binding protein mXBp - mouse (fragment)	Qy	145 NR 146 : 	
C;Species: Mus musculus (house mouse)	Db	188 NR 189		
C;Sequence_change 13-Jul-1990 #text_change 26-Aug-1999				
C;Accession: A34785				
R;Ivashkiv, L.B.; Liou, H.C.; Kara, C.J.; Lamph, W.W.; Verma, I.M.; Glimcher, L.H.				
Mol. Cell. Biol. 10, 1609-1621, 1990				
A;Title: mXBp/CRE-BP2 and c-Jun form a complex which binds to the cyclic AMP, but not to a complex which binds to the cyclic AMP, but not to				
A;Reference number: A34785; MUID: 90205841; PMID: 2138707				
A;Status: preliminary				
A;Molecule type: mRNA				
A;Residues: 1-313 <R>				
A;Cross-references: UNIPARC:UPI000016CP39; GB:M31629; NID:919926; PIDN:AAA39780_1; PID: F155-195; Domain: fos/jun DNA-binding domain homology <FJD>				
Query Match Score 170; DB 2; Length 313;				
Best Local Similarity 50.0%; Pred. No. 3.8e-07;				
Matches 39; Conservative 6; Mismatches 7; Indels 26; Gaps 3;				
Qy 57 PARNSKIEEPSVETTHQDSPLPHPESTSDEKEVPLAQTAAOPTSALIVRPAQLQVNVL 116	Qy 2 KPKLHNNSARQYKDLKWNMSDDKPKPELTAPCGCORTPNEDHLAVHKHHEMTLKFGG----- 57			
Db 23 PIRSKIEEPSVETTHQDSPLPHPESTSDEK-----LVRPVTM-VPSV- 66	Db 286 KXKL-TNHIRVH-----TCGKPPCPFPFGCKVPARSENKIKRHTHGEKPKFCBEG 338			
Qy 117 TSSDSSYLIQQAVPSPTS 134	Qy 58 -----ARNSKIEEPSVETHQ-----DSPLPHPESTSDEK-EVPLAQTAQPSAIV 104			
Db 67 -----PGIPGSS 74	Db 339 CDRRFFANSDRKGKMHVHTSDKPVLCKMKCUDSYTBSURKHMVKYHESSSGSOPSPA-- 396			
Qy 397 -----ASSGYESSTTPPTIVSPPTDNPTISSM--SPSSSS 427	Qy 105 RPASLQPVNTLTSQSSVLIQQAVESPSTSSTVITQAPSSN 145			
RESULT 10				
T43532	Zinc finger protein rsv1 - fission yeast (Schizosaccharomyces pombe)	Qy 105 RPASLQPVNTLTSQSSVLIQQAVESPSTSSTVITQAPSSN 145		
C;Species: Schizosaccharomyces pombe	Db 339 CDRRFFANSDRKGKMHVHTSDKPVLCKMKCUDSYTBSURKHMVKYHESSSGSOPSPA-- 396			
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Feb-2000				
C;Accession: T43532				
R;Hao, Z.; Furunobu, A.; Nagata, A.; Okayama, H.				
J. Cell. Sci. 110, 2557-2566, 1997				
A;Title: A zinc finger protein required for stationary phase viability in fission yeast.				
A;Reference number: 222548; MUID: 98039713; PMID: 9372444				
A;Accession: T43532				
A;Status: preliminary				
A;Molecule type: DNA				
A;Residues: 1-428 <RHA>				
A;Cross-references: UNIPARC:UPI00001687F4; EMBL:AF016222; PIDN:AA887047.1				
A;Experimental source: strain 972h(-)				
C;Function:				
A;Genes: rsv1				
A;Description: required for cell viability in a stationary phase induced by glucose star				
Query Match Score 113; DB 2; Length 428;				
Best Local Similarity 21.4%; Pred. No. 0.037;				
Matches 39; Conservative 20; Mismatches 65; Indels 58; Gaps 4;				
Qy 12 QYKDLWNMSDDKPKFLCTAPGCGORTPNEDHLAVHKHHEMTLKFGPARNSKIEEPSVET 71	Qy 9 SARQYDLMNN-SDDCPFLCTAPGCGORTPNEDHLAVHKHHEMTLKFGPARNSKIEEPSVET 71			
Db 19 QVRHIRSHTEGKFECPSCKGRFTRDELTHVVRTH-----LRKALVTPEQTLDV 70	Db 298 SATNYQHVRHTGGBPvYvCvTGPCKRFTEYSSLNHDVvTHCPRYTCSITCGKTYROT 357			
Qy 72 THQDSPLPHPESTSDEKEVPLAQT-----AQPTSAIVRPAVL 109	Qy 42 -LAVHKHHEMTLKFGPARNSKIEEPSVETHQDSPLPHPE-----STTSDBKEVP 92			
Db 71 NLHTAPDSKPEGDKSTGQDAKSQNQSIXGTSITDPVQAVIALSVAKPTSVLSPTDL 130	Db 358 STLAMKRSANGELETEEESQALYQQQLEAASAAEESPPPEKRPIAYLSEVEKERDDI 417			
Qy 110 QVNPVLLT-----SSDSVVIQQAQVSPSTSITVITQAPS 144	Qy 93 LRQTAOPTSAIVRPAVLQVNPVLLTSSVIIQQAQVSPSTSITVITQAPS 143			
Db 131 QAQSKLIEKPRRRSASATGSLNKNDQPLRRFSISSEAGAAAAPTSPSNS--KSPPS 187				

Db	418 FAQVAMVTE-----EDGAPQVALITQDGAA---QQVTIITSGAVVABDSS 458
RESULT 13	T38743 hypothetical zinc finger protein - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T38743 R;Genes: S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. Submitted to the EMBL Data Library, December 1995 A;Reference number: 221808 A;Accession: T38743 A;Status: preliminary; translated from GB/EMBL/DBJ A;Molecule type: DNA A;Residues: 1-562 <GEN> A;Cross-references: UNIPROT:Q10076; UNIPARC:UPI00013A12B; EMBL:Z68144; PIDN:CA C;Genetics: A;Gene: SPAC3H1.11 A;Map position: 1
	Query Match Score 13.8%; DB 2; Length 582; Best Local Similarity 26.7%; Pred. No. 0.17; Gaps 6; Matches 39; Conservative 21; Mismatches 62; Indels 24; Gaps 6;
Qy	2 KFKLHNSARQYKDLNMMSDDKPFCLTAPPGCGQRFNTNDHLAVHKHXHEMLTKFGPARN 61
Db	431 KFKRSFHRRHSL--HTSEKEPVFCI---CGFRFSRDNLRQHERLH--VNASP-RLA 481
Qy	62 KIEEPSPVETTHQDPSLPHPESTTSDEKEVPLAQTAQPTSATVRPASLQVPNVNTLSSDS 121
Db	482 CFFQPQSYSSGGAPAVQPKQPIEDLNKIPINQMD-----SSQIENTNLMLSSQ 532
Qy	122 SVIQQAVPSPSTSIVTQAPSNNRP 147
Db	533 RPLSQIQVPE-----IAAYPNISR P 552
RESULT 14	A49839 odd-paired - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004 C;Accession: A49839 R;Benedyk, M.J.; Mullon, J.R.; DiNardo, S. Genes Dev. 8, 105-117, 1994 A;Title: odd-paired: a zinc finger pair-rule protein required for the timely activation of even-skipped A;Reference number: A49839; MUID:94116854; PMID:8288124 A;Accession: A49839 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-609 <GEN> A;Cross-references: UNIPROT:P39768; UNIPARC:UPI000130D63; GB:U04435; NID:94373 C;Genetics: A;Gene: opa A;Cross-references: FlyBase:FBgn0003002 C;Keyword: zinc finger
	Query Match Score 13.3%; DB 2; Length 609; Best Local Similarity 24.9%; Pred. No. 0.4; Gaps 7; Matches 43; Conservative 23; Mismatches 67; Indels 40; Gaps 7;
Qy	2 KPKLHNSARQYKDLNMMSDDKPFCLTAPPGCGQRFNTNDHLAVHKHXHEMLTKFGP-----57
Db	275 KYKL-YNHIRH-----TGEPFACPHRPGCGKVRPARENKLKHRTGTGEKPKCEHEG 327
Qy	58 -----ARNSKLBPSPVETTHQDPSLPHPESTTS-----DSPLPABESTS-----DEKEVPLAQ 95
Db	328 CDRRFANNSDRKKHSHVHTSDKPYNCRINGCDKSYTBPSSLLKMMKVHGNYVDEKSPSHGY 387
Qy	96 TAA----PTSA1TVRPAQSVQPVNTLTSQDSSVIIQDAPSPSTSSTVTOAPSS 144

Fri Jan 13 09:47:01 2006

aah26175.rpr

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Search completed: January 10, 2006, 23:06:56
Job time : 18 secs

Page 1

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 protein search, using sw model
 on: January 10, 2006, 23:00:17 ; Search time 71 Seconds
 (without alignments)
 1480.616 Million cell updates/

 title: AAH26175
 subject: 776
 sequence:
 1 mkfkhvnsarqykdlwwm8.....ppptasrtvitqapsenpriv 149

Scoring table: BLOSUM62
 Gapopen 10.0 , Gapext 0.5
 Searched: 2166443 seqs, 705528306 residues
 Actual number of hits satisfying chosen parameters: 2166443

minimum DB seq length: 0
maximum DB seq length: 200000000
post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

database : UniProt_05_80:
1: uniprot_sprot:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
15	736	94.8	209	2	Q8TARI	HUMAN
2	736	94.8	505	2	Q4RTZ2	MACACA F
3	636	82.0	234	2	Q8BN75	_MOUSE
4	636	82.0	420	2	Q8CBR9	_MOUSE
5	636	82.0	487	1	ATF2	_HUMAN
6	636	82.0	487	2	ATF2	_MOUSE
7	636	82.0	487	2	Q8CBB4	_MOUSE
8	632	81.4	487	1	ATF2	_RAT
9	612	78.9	487	1	ATF2	_CHICK
10	594	76.5	486	2	Q91576	XENOPUS
11	445	57.3	440	2	Q68FB3	_MOUSE
12	445	57.3	447	2	Q544G2	_MOUSE
13	366	47.2	389	2	Q64016	_MOUSE
14	300	38.7	413	1	ATF7	_MOUSE
15	295	38.0	483	1	ATF7	_PONY
16	289.5	37.3	413	2	Q4RAX6	TETRAODON
17	289.5	37.3	494	1	ATF7	_HUMAN
18	273.5	35.9	497	2	Q4VGW9	_BRAEVE
19	273.5	35.2	427	2	Q4VQW8	_BRAEVE
20	268.5	34.6	148	2	Q75NO2	_HUMAN
21	260.5	33.6	508	1	CREB5	_HUMAN
22	253	32.6	540	2	Q4RYW6	TETNG
23	235	30.3	307	2	Q9IDB3	_HUMAN
24	224	28.9	144	2	Q96DT8	_HUMAN
25	221	28.5	525	2	Q4RHY0	_TESTING
26	213	27.4	117	2	Q8IVTR8	_HUMAN
27	181.5	23.4	61	2	Q4RNQ7	_TESTING
28	168	21.6	135	2	Q8RK9N	MOUSRE
29	168	21.6	144	2	Q8BM42	_MOUSE
30	159.5	20.6	571	2	Q4SIX1	_TESTING
31	138	17.8	23	2	Q53RV7	_HUMAN

3.2	135.5	17.5	226	Q4H3W0_CIOIN	Q4h3w0 ciona intes
3.3	135.5	17.5	631	Q4H3W1_CIOIN	Q4h3w1 ciona intes
3.4	116.5	15.0	396	Q4FMB7_CANGA	Q4fmB7 candida gla
3.5	116	14.9	717	Q55NQ1_CRTNB	Q55nq1 cryptococcu
3.6	115.5	14.9	509	Q4PG17_USTMIA	Q4pg17 ustilago ma
3.7	114	14.8	503	Q9NAR8_BRAFL	Q9nar8 brachiosco
3.8	113	14.6	428	RSV1_SCBPO	Q9p7d9 schizosacch
3.9	113	14.6	568	Q8BMF0_MOUSB	Q8bmf0 mus musculu
4.0	111	14.4	1354	Q9W6B2_XENLIA	Q9w6z9 xenopus lae
4.1	111.5	14.4	1553	Q6U6Z3_BRARE	Q6u6z9 brachydanio
4.2	111	14.3	183	Q9PVD6_BRARE	Q9pvd6 brachydanio
4.3	111	14.3	442	O93311_BRARE	O93311 brachydanio
4.4	111	14.3	691	Q5KC36_CRYTCCU	Q5kc36 crytrococcu
4.5	110	14.2	303	Q6UNK5_BOVIN	Q6unk5 bos taurin

סימני זיהוי

RTF generation and initial analysis of more than 12,000 full
 RLU and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [2]
 RPL NUCLEOTIDE SEQUENCE.
 RPS TISSUE-Skin.
 RRC STRAUSBERG R.;
 RLU Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: FC026175; AAH26175.1; -; mRNA.
 DR HS336; P15336; 1B1H.
 DR Ensemble: ENSC00000115966; Homo sapiens.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO; GO:0014682; F:metal ion binding; IEA.
 DR GO; GO:0003576; F:nucleic acid binding; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR InterPro; IPR007087; Znf_C2H2.
 DR SMART; SFM00355; zf-C2H2_1.
 DR PROSITE; PS00096; zf-C2H2_1.
 DR PROSITE; PS550157; ZINC_FINGER_C2H2_1.
 DR PROSITE; PS550157; ZINC_FINGER_C2H2_2.
 DR PROSITE; PS550157; ZINC_FINGER_C2H2_2.

KW	Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SQ	SEQUENCE 209 AA; 23050 MW; A26AF07CH5D8DSE7 CRC64;
Query Match	94.8%; Score 736; DB 2; Length 209;
Best Local Similarity	71.3%; Pred. No. 8e-51;
Matches	149; Conservative 0; Mismatches 0; Indels 60; Gaps 1;
Qy	1 MKFKLHYNSARQYKDLWNMSDDKPKFLCTAPGGQRTNEVDHLAVHGHKHMTLKGFPARN 60
Db	1 MKFKLHYNSARQYKDLWNMSDDKPKFLCTAPGGQRTNEVDHLAVHGHKHMTLKGFPARN 60
Qy	61 -----
Db	61 DSIVIADQTPTRFLKNCCEYGLFNLASPPNEFEKKASEDDIKKMPPLDLSPLATPIIR 120
Qy	61 SKIEEPSSVETHDQSPSLPHPESTTSDEKEVPLAQTAAQPTSAIVPASLQVNVLITSSD 120
Db	121 SKIEEPSSVETHDQSPSLPHPESTTSDEKEVPLAQTAAQPTSAIVPASLQVNVLITSSD 180
Qy	121 SSVIQQAVPSPTSSVTQTAQPSNRPIV 149
Db	181 SSVIQQAVPSPTSSVTQAPSNNRPIV 209
RESULT 2	
Q4R5T2	MACPA ID Q4R5T2_MACPA PRELIMINARY;
AC	31 (TREMBLrel. 31, Created)
DT	15-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT	13-SEP-2005 (TREMBLrel. 31, Last annotation update)
RA	Testis cDNA, clone: Qtsa_21051, similar to human activating transcription factor 2 (ATF2), OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaert P., Nordne P., Ring B., Rinewat M., Rodriguez I., Samamoto N., Sasaki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F., RA Wynshaw-Boris P., Yoshida K., Hasegawa Y., Kawaji H., Kohtsubuki S., RA Hayashizaki Y., Hirata M., Kubuda J., Hida M., Suzuki Y., RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hämäläinen K., RT "DNA sequences of macaque genes expressed in brain or testis and its evolutionary implications.", Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RL	Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RN	NUCLEOTIDE SEQUENCE.
RA	Osada N., Hirata M., Tanuma R., Kubuda J., Hida M., Suzuki Y., Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hämäläinen K., RT "Substitution rate and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey cDNAs.", Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AB169461; BAE01543.1; -; mRNA.
SQ	SEQUENCE 505 AA; 54507 MW; 01905EFAEC924B67 CRC64;
Query Match	94.8%; Score 736; DB 2; Length 505;
Best Local Similarity	71.3%; Pred. No. 2.3e-51;
Matches	149; Conservative 0; Mismatches 0; Indels 60; Gaps 1;
Qy	1 MKFKLHYNSARQYKDLWNMSDDKPKFLCTAPGGQRTNEVDHLAVHGHKHMTLKGFPARN 60
Db	1 MKFKLHYNSARQYKDLWNMSDDKPKFLCTAPGGQRTNEVDHLAVHGHKHMTLKGFPARN 60
Qy	61 -----
Db	61 DSIVIADQTPTRFLKNCCEYGLFNLASPPNEFEKKASEDDIKKMPPLDLSPLATPIIR 120
Qy	61 SKIEEPSSVETHDQSPSLPHPESTTSDEKEVPLAQTAAQPTSAIVPASLQVNVLITSSD 120
Db	121 SKIEEPSSVETHDQSPSLPHPESTTSDEKEVPLAQTAAQPTSAIVPASLQVNVLITSSD 180
Qy	121 SSVIQQAVPSPTSSVTQAPSNNRPIV 149
Db	181 SSVIQQAVPSPTSSVTQAPSNNRPIV 209

RESULT 3	
Q8BN75	MOUSE PRELIMINARY;
ID Q8BN75_MOUSE	PRT; 234 AA.
AC Q8BN75;	CREATED)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)	(TREMBLrel. 23, Last annotation update)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)	Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone: E130020102 product:activating transcription factor 2, full insert sequence.
DE [1]	DE library. clone: E130020102 product:activating transcription factor 2, full insert sequence.
GN Name-At:f2;	
OS Mus musculus (Mouse).	
OU Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathia; Muroidea; Muridae; Murinae; Mus.	
OC NCBI_TaxID=10090;	
RN RN	
NUCLEOTIDE SEQUENCE.	
RP STRAIN=C57BL/6J; TISSUE=Eyeball;	
RC RC	
MDLINE=21085650; PubMedId=121751;	DOI=10.1038/35055500;
RX RX	
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaert P., Nordne P., Ring B., Rinewat M., Rodriguez I., Samamoto N., Sasaki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F., RA Wynshaw-Boris P., Yoshida K., Hasegawa Y., Kawaji H., Kohtsubuki S., RA Hayashizaki Y., Hirata M., Kubuda J., Hida M., Suzuki Y., RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hämäläinen K., RT "Functional annotation of a full-length mouse cDNA collection.", RA "Analysis of the mouse transcriptome based on functional annotation of [3] cDNAs.", RA Nature 409:685-690 (2001); RA Nucleotide Sequence.	
RP STRAIN=C57BL/6J; TISSUE=Eyeball;	
RC RA	
RA The RIKEN Genome Exploration Research Group Phase I & II Team;	The RIKEN Genome Exploration Research Group Phase I & II Team;
RA MEDLINE=2049934; PubMedId=1012159;	DOI=10.1101/gr.145100;
RX RA	
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; RA "Normalization and subtraction of cap-trapper-selected cDNAs to RT prepare full-length cDNA libraries for rapid discovery of new genes.";	"Normalization and subtraction of cap-trapper-selected cDNAs to RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RN RN	
NUCLEOTIDE SEQUENCE.	
RP STRAIN=C57BL/6J; TISSUE=Eyeball;	
RC RA	
RA "Analysis of the mouse transcriptome based on functional annotation of new genes.";	"Analysis of the mouse transcriptome based on functional annotation of new genes.";
RA MEDLINE=2053093; PubMedId=107861;	DOI=10.1101/gr.152600;
RX RA	
RX Carninci P., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Tashiro H., Itoh M., RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., RA	

Page 4

FT DOMAIN	362	390	Leucine-zipper.
FT ZN FING	7	31	C2H2-type.
FT DNA BIND	333	356	Basic motif.
FT MOD-RES	51	51	Phosphothreonine (by MAPK14).
FT MOD-RES	51	53	Phosphothreonine (by MAPK14).
FT MOD-RES	53	53	Phosphoserine.
FT MOD-RES	94	94	Missing (in isoform 2).
FT VARSPLIC	1	158	/FTID=SP_000587.
FT VARSPLIC	159	167	TSSDSSVII -> MSTAYFQMM (in isoform 2).
FT CONFFLICT	191	191	/FTID=VSP_000588.
FT CONFLICT	205	205	V -> L (in Ref. 2).
FT CONFLICT	293	293	N -> S (in Ref. 1).
FT TURN	2	3	R -> L (in Ref. 2).
FT STRAND	7	8	
FT TURN	12	14	
FT STRAND	17	18	
FT HELIX	21	32	
FT TURN	33	37	
SQ SEQUENCE	487 AA;	52277 MW;	58ADD6240D6270E8 CRC64;
Query Match			Score 636; DB 1; Length 487;
Best Local Similarity			Pred. No. 2e-42;
Matches 131;			Mismatches 0; Indels 1;
Qy	19	MSDDKPFILC TAPGCGG RTNFEDHLAVKH KHEMTLKF GPARN-----	60
Db	1	MSDDKPFILC TAPGCGG RTNFEDHLAVKH KHEMTLKF GPARNSVADQPTPFRFLQN	60
Qy	61	----- SKI E P S Y V E T T H Q D S P I 78	
Db	61	CBEVGLFNE LASPFENEFK KASEDDIKRMPUDLSPLATPLRSKIE P S V E T T H Q D S P I 120	
Qy	79	PHPESTTSDEKEVPLAQTAQPSATIVRPA S L Q V P N V L T T S D S V V I O Q A V P S P T S S V I 138	
Db	121	PHPESTTSDEKEVPLAQTAQPSATIVRPA S L Q V P N V L T T S D S V V I O Q A V P S P T S S V I 180	
Qy	139	TQAPSNNRPIV 149	
Db	181	TQAPSNNRPIV 191	
RESULT 6			
ID ATF2_MOUSE		STANDARD; PRT;	487 AA.
AC P16851; Q64089; Q64090; Q64091;			
DT 01-AUG-1990 (Rel. 15, Created)			
DT 30-MAY-2000 (Rel. 39, Last sequence update)			
DT 13-SEP-2005 (Rel. 48, Last annotation update)			
DE "Functionally distinct isoforms of the CRE-BP transcription factor ATF-2 (Activating transcription factor 2) (cAMP response element binding protein CRE-BP1) (MAPBP protein)."			
GN Names=Atf2;			
OS Mus musculus (Mouse)			Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia; Sciurognathi; Mucoidea; Muridae; Murinae; Mus.
OC			
NCBI_TaxID=10090;			
RN [1]			NUCLEOTIDE SEQUENCE OF 9-487, AND ALTERNATIVE SPLICING.
RX MEDLINE=92123199; PubMed=1531087;			
RA Georgopoulos K.; Morgan B.A.; Moore D.D.;			"Functionally distinct isoforms of the CRE-BP DNA-binding protein mediate activity of a T-cell-specific enhancer.";
RT Mol. Cell. Biol. 12:747-757 (1992).			
RN [2]			NUCLEOTIDE SEQUENCE (ISOFORM 1).
RP STRAIN=IIS, and ISS;			MEDLINE=11363810; PubMed=11471062; DOI=10.1007/s00335-001-1001-x;
RX Ehringer M.A.; Thompson J.; Conroy O.; Xu Y.; Yang F.; Canniff J.;			
RA Beeson M.; Gordon L.; Bennett B.; Johnson T.E.; Sikela J.M.;			"High-throughput sequence identification of gene coding variants within alcohol-related QTLs."
RT			
RL Mamm. Genome 12:657-663 (2001).			
RN [3]			
RP NUCLEOTIDE SEQUENCE OF 77-487.			
RX MEDLINE=90205861; PubMed=2138707;			
RA Ivassisiv L.B.; Liou H.-C.; Kara C.J.; Lamph W.W.; Verma I.M.;			
RA Glincher L.H.;			
RT "mXBp/CRE-BP2 and c-Jun form a complex which binds to the cyclic AMP, but not to the 12-O-tetradecanoylphorbol-13-acetate response elements (TRES) as part of an MXBP-c-Jun element."			
RT Mol. Cell. Biol. 10:1609-1621 (1990).			
CC -1- FUNCTION: A transcriptional activator, probably constitutive, which binds to the cAMP responsive region (CRE) (consensus: 5'-GTGACCT[AC] [AG]-3') ; a sequence present in many viral and cellular promoters. The interaction of MXBP/CRE-BP2 with JUN redirects JUN to bind to CREs preferentially over the 12-O-tetradecanoylphorbol-13-acetate response elements (TRES) as part of an MXBP-c-Jun complex.			
CC -1- SUBUNIT: Binds DNA as a dimer and can form a homodimer with JUN.			
CC -1- absence of DNA. Can form a heterodimer with JUN.			
CC -1- SUBCELLULAR LOCATION: Nuclear.			
CC -1- ALTERNATIVE PRODUCTS:			
CC Event=Alternative splicing; Named isoform=3;			
CC Name=1;			
CC IsoId=P16951-1; Sequence=Displayed;			
CC Name=2;			
CC IsoId=P16951-2; Sequence=VSP_000590;			
CC Name=3;			
CC IsoId=P16951-3; Sequence=VSP_000589;			
CC -1- SIMILARITY: Belongs to the bZIP family. ATP subfamily.			
CC -1- SIMILARITY: Contains 1 bZIP domain.			
CC -1- SIMILARITY: Contains 1 C2H2-type zinc finger.			
CC This Swiss-Prote entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
CC -----			
DR EMBL; S76657; AAB21128.1; ALT INT1; mRNA.			
DR EMBL; S76655; AAB21129.1; ALT INT1; mRNA.			
DR EMBL; S76655; AAB21127.1; -; mRNA.			
DR AF483482; AAU90756.1; -; mRNA.			
DR AF483483; AAU90757.1; -; mRNA.			
DR M31629; AAA39780.1; -; mRNA.			
DR HSSP; P15336; 1BHI.			
DR SMR; P16951; 336-336.			
DR TRANSFAC; T01017;			
DR Ensemble; ENSMUSG00000027104; Mus musculus.			
DR MGI; MGI:109349; Af2.			
DR GO; GO:0005677; P:DNA binding, IDA.			
DR GO; GO:0005515; F:protein binding, IPI.			
DR InterPro; IPR011616; bZIP 1.			
DR InterPro; IPR004827; Znf_C2H2.			
DR InterPro; IPR007087; Tf_bZIP.			
DR Pfam; PF00170; bZIP 1; 1.			
DR Pfam; PF00096; zf-C2H2 1.			
DR SMART; SM00338; BRIZ2; 1.			
DR SMR; SM00355; Znf_C2H2; 1.			
DR PROSITE; PS50217; BZIP 1.			
DR PROSITE; PS00036; BZIP BASIC; 1.			
DR PROSITE; PS00028; ZINC_FINGER_C2H2 1; 1.			
DR PROSITE; PS50157; ZINC_FINGER_C2H2 2; 1.			
KW Activator; Alternative splicing; DNA-binding; Metal-binding; Nuclear protein; Phosphorylation; Transcription; Zinc-finger.			
KW Transcription regulation; Zinc; Zinc-finger; Leucine-zipper.			
FT DOMAIN	362	390	C2H2-type.
FT DNA_BIND	333	356	Basic motif.
FT MOD_RBS	51	51	Phosphothreonine (by MAPK14) (By similarity).
FT MOD_RES	53	53	Phosphothreonine (by MAPK14) (By similarity).
FT MOD_RES	94	94	Phosphoserine (By similarity).

FT	VARSPLIC	1	48	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR NDSEVIVA -> NHCPWVWP (in isoform 3).	RL	Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
FT	/FTID=VSP	000590.		/FTID=VSP (In isoform 2).	DR	EMBL: BC042210; AAH42210-1; -; mRNA.
FT	MISSING	229		Missing (In isoform 2).	DR	HSSP; P15236; 1BHT.
FT	/FTID=VSP	000590.		/FTID=VSP -_AQPSGS -> HSPOEV (in Ref. 1).	DR	SMR; Q8GBA; 336-396.
FT	CONFLICT	482	487	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR SEQUENCE 487 AA; 52298 MW;	DR	MGI; MGI:109349; At:2.
SQ	SEQUENCE	131;	Conservative	Score 636; DB 1; Length 487; Best Local Similarity 68.6%; Pred. No. 2e-42; 0; Mismatches 0; Indels 60; Gaps 1;	GO	GO:0003677; P:DNA binding; IDA; GO; GO:000515; P:protein binding; IPI.
Qy	Query Match	19	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR DB	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR 1 MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR 61 -----SKIERPSVVTTHODSP-----78	DR	InterPro; IPR01616; bZIP 1.
Qy	Qy	61	-----PHEESTSDEKEVPLAQPATPSVTTKPSKIEBSVVTTHODSP-----120	DR	InterPro; IPR004827; TF_HZIP. InterPro; IPR007087; zf_C2H2. PFam; PF00170; bZIP 1; PFam; PF00096; zf-CPH2; 1.	
Db	Db	61	CEEVGLFNLASPPNEPEPKASDDIKMPLDLSPLATPLPSKIEBSVVTTHODSP-----60	DR	SMART; SM00338; BRLZ_1. SMART; SM00355; Znf_C2H2; 1.	
Qy	Qy	79	PHEESTSDEKEVPLAQPATPSVTTKPSKIEBSVVTTHODSP-----138	DR	PROSITE; PS50217; BZIP_P; 1.	
Db	Db	121	PHEESTSDEKEVPLAQPATPSVTTKPSKIEBSVVTTHODSP-----180	DR	PROSITE; PS50036; BZIP_BASIC; 1.	
Qy	Qy	139	TOAPSNSRPIV 149	DR	PROSITE; PS50028; ZINC_FINGER_C2H2; 1.	
Db	Db	181	TOAPSNSRPIV 191	DR	PROSITE; PS50157; ZINC_FINGER_C2H2; 2.	
RESUL	7	8	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	SQ	SEQUENCE 487 AA; 52310 MW; FA2B093BC210CFCB CRC64;	
QBCGB4	MOUSE		Query Match 82.0%; Score 636; DB 2; Length 487; Best Local Similarity 68.6%; Pred. No. 2e-42; 0; Mismatches 0; Indels 60; Gaps 1;	Qy	Query Match 82.0%; Score 636; DB 2; Length 487; Best Local Similarity 68.6%; Pred. No. 2e-42; 0; Mismatches 0; Indels 60; Gaps 1;	
QBCGB4	-		Matches 131;	Qy	Matches 131;	
AC	QBCGB4_-		PROSITE; PS50217; BZIP_P; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
DT	01-MAR-2003	(TREMBLrel. 23,	PROSITE; PS50036; BZIP_BASIC; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
DT	01-MAR-2003	(TREMBLrel. 23, Last sequence update)	PROSITE; PS50028; ZINC_FINGER_C2H2; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)	PROSITE; PS50157; ZINC_FINGER_C2H2; 2.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
DE	Atf2 Protein.		PROSITE; PS50217; BZIP_P; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
GN	Name=Atf2;		PROSITE; PS50036; BZIP_BASIC; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
OS	Mus musculus (Mouse).		PROSITE; PS50028; ZINC_FINGER_C2H2; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		PROSITE; PS50157; ZINC_FINGER_C2H2; 2.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		PROSITE; PS50217; BZIP_P; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
NCBI_TAXID=10090;			PROSITE; PS50036; BZIP_BASIC; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RN	[1]		PROSITE; PS50028; ZINC_FINGER_C2H2; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RP	NUCLEOTIDE SEQUENCE.		PROSITE; PS50157; ZINC_FINGER_C2H2; 2.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RC	STRAIN=CZECH II;		PROSITE; PS50217; BZIP_P; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RC	TISSUE=Mammalian tumor metastatized to lung. Tumor arose spontaneously;		PROSITE; PS50036; BZIP_BASIC; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		PROSITE; PS50028; ZINC_FINGER_C2H2; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,		PROSITE; PS50157; ZINC_FINGER_C2H2; 2.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Shamnen R.D., Collins F.S., Wagner L., Schuler G.D.,		PROSITE; PS50217; BZIP_P; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,		PROSITE; PS50036; BZIP_BASIC; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile P.,		PROSITE; PS50028; ZINC_FINGER_C2H2; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		PROSITE; PS50157; ZINC_FINGER_C2H2; 2.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		PROSITE; PS50217; BZIP_P; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		PROSITE; PS50036; BZIP_BASIC; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Barua S.S., Loqueilano N.A., Peters J., Abramson D., Mullany S.J.,		PROSITE; PS50028; ZINC_FINGER_C2H2; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Basak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gundarathne P.H.,		PROSITE; PS50157; ZINC_FINGER_C2H2; 2.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		PROSITE; PS50217; BZIP_P; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Villanova D.K., Muzy D.M., Sodergren B.J., Lu X., Gibbs R.A.,		PROSITE; PS50036; BZIP_BASIC; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Fahey J., Heiton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,		PROSITE; PS50028; ZINC_FINGER_C2H2; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		PROSITE; PS50157; ZINC_FINGER_C2H2; 2.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		PROSITE; PS50217; BZIP_P; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Rodriguez A.C., Grimes J., Schmutz J., Myers R.M.,		PROSITE; PS50036; BZIP_BASIC; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E.,		PROSITE; PS50028; ZINC_FINGER_C2H2; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.,		PROSITE; PS50157; ZINC_FINGER_C2H2; 2.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RT	"Genomic and initial analysis of more than 15,000 full-length human		PROSITE; PS50217; BZIP_P; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RT	and mouse cDNA sequences.";		PROSITE; PS50036; BZIP_BASIC; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		PROSITE; PS50028; ZINC_FINGER_C2H2; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RN	[2]		PROSITE; PS50157; ZINC_FINGER_C2H2; 2.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RP	NUCLEOTIDE SEQUENCE.		PROSITE; PS50217; BZIP_P; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RC	STRAIN=CZECH II;		PROSITE; PS50036; BZIP_BASIC; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RC	TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;		PROSITE; PS50028; ZINC_FINGER_C2H2; 1.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	
RA	Strausberg R.		PROSITE; PS50157; ZINC_FINGER_C2H2; 2.	Db	MSDDDKPFLCTAPGGCQRFNTEDHLAVRKHKHEMTLKGPAR-----60	

cc	GTTGAACTT[AC] [AG] -3'), a sequence present in many viral and cellular promoters.	Db	181 TQAPSSNRPIV 191
cc	- - SUBUNIT: Binds DNA as a dimer.		
cc	- - SUBCELLULAR LOCATION: Nuclear.		
cc	- - ALTERNATIVE PRODUCTS:		
cc	Event=Alternative splicing; Named isoform=2;		
cc	Name=1;		
cc	IsoId=Q00969-1; Sequence=Displayed;		
cc	Name=2;		
cc	IsoId=Q00969-2; Sequence=VSP_000991;		
cc	- - SIMILARITY: Belongs to the bZIP family. ATF subfamily.		
cc	- - SIMILARITY: Contains 1 bZIP domain.		
cc	- - SIMILARITY: Contains 1 C2H2-type Zinc finger.		
cc	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.		
cc	TRANSFAC: T01382; -		
cc	DR Ensembl: ENSRNOG0000000001597; Rattus norvegicus.		
cc	DR EMBL: U38938; AAA91263.1; - ; mRNA.		
cc	DR EMBL: M61148; AAA4013.1; - ; mRNA.		
cc	DR PIR: A39429; A39429.		
cc	DR HSSP; P13336; 1BHI.		
cc	DR SMR; Q0069; 336-306.		
cc	DR InterPro: IPR011616; bZIP 1.		
cc	DR InterPro: IPR004827; TF bZIP.		
cc	DR InterPro: IPR007082; Znf_C2H2.		
cc	DR Pfam: PF00170; bZIP 1.		
cc	DR Pfam: PF00096; zf-C2H2; 1.		
cc	DR PROSITE: PS00501; bZIP; 1.		
cc	DR PROSITE: PS00028; ZINC FINGER C2H2; 1; 1.		
cc	DR PROSITE; PS0036; ZINC FINGER C2H2; 1; 1.		
cc	DR PROSITE; PS00157; ZINC_FINGER_C2H2; 1; 1.		
cc	KW Activator; Alternative splicing; DNA-binding; Metal-binding; Nuclear Protein; Phosphorylation; Transcription; Transcription regulation; Zinc; Zinc-finger.		
cc	KW KW		
cc	FT DNAIN 362 390 Leucine-zipper.		
cc	FT ZN_FING 7 31 C2H2-type.		
cc	FT DNA_BIND 333 356 Basic motif.		
cc	FT MOD_RES 51 51 Phosphothreonine (by MAPK14) (By similarity).		
cc	FT MOD_RES 53 53 Phosphothreonine (by MAPK14) (By similarity).		
cc	FT MOD_RES 94 94 Phosphoserine (By similarity).		
cc	FT VARSPPLIC 132 229 Missing (in isoform 2).		
SQ	SEQUENCE 487 AA; 52287 MW; 4E995B1G6DF559EE CRC64;		
cc	Query Match 81.4%; Score 632. DB 1; Length 487; Best Local Similarity 67.5%; Pred. No. 4.1e-42; Matches 129; Conservative 2; Mismatches 0; Indels 60; Gaps 1;		
cc	KW Activator; DNA-binding; Metal-binding; Nuclear protein; Transcription; Leucine-zipper.		
cc	KW DOMAIN 362 390 C2H2-type.		
cc	FT ZN_FING 7 31 Basic motif.		
cc	FT DNA_BIND 333 356 MW; AlFP42734D9C6A146 CRC64;		
cc	FT SEQUENCE 487 AA; 52287 MW; 4E995B1G6DF559EE CRC64;		
cc	Query Match 78.9%; Score 612; DB 1; Length 487; Best Local Similarity 65.4%; Pred. No. 1.6e-40; Matches 125; Conservative 3; Mismatches 3; Indels 60; Gaps 1;		
Qy	19 MSDDKPFLCTAPGGCGQRTEDHIAVHKHKGMLKFGPARN-----	Db	19 MSDDKPFLCTAPGGCGQRTEDHIAVHKHKGMLKFGPARN-----
Qy	1 MSDDKPFLCTAPGGCGQRTEDHIAVHKHKGMLKFGPARN-----	Db	1 MSDDKPFLCTAPGGCGQRTEDHIAVHKHKGMLKFGPARN-----
Qy	79 PHPESTTSDEKEVPLAQTAOPTSAIVRPAQLQPNVLTSDDSSVVIQAVPSPSSVTI 138	Db	121 PHPESTTSDEKEVPLAQTAOPTSAIVRPAQLQPNVLTSDDSSVVIQAVPSPSSVTI 180
Qy	139 TOAPSSNRPIV 149	Qy	61 -----SKLEEPSVETTHQDSPL 78
Qy	61 CEEVGLFNELASPPFENEFKASEDDIKMPLDLSPATPIRSKEEPSVETTHQDSPL 120	Db	61 CEEVGLFNELASPPFENEFKASEDDIKMPLDLSPATPIRSKEEPSVETTHQDSPL 120
Qy	79 PHPESTTSDEKEVPLAQTAOPTSAIVRPAQLQPNVLTSDDSSVVIQAVPSPSSVTI 138	Db	121 PHPESTTSDEKEVPLAQTAOPTSAIVRPAQLQPNVLTSDDSSVVIQAVPSPSSVTI 180
Qy	139 TOAPSSNRPIV 149	Qy	61 -----SKIEPSVETTHQDSPL 78

- Qy 123 VIQQAVPSPSSSTVTOAPSNNRPIY 149
Db 125 VIQQAVPSPSSSTVTOAPSNNRPIY 151
- RESULT 12
Q54G2_MOUSE
ID Q54G2_MOUSE PRELIMINARY;
AC Q54G2;
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D13059A07 product:activating transcription factor 2, full insert sequence.
DE Name=Atf2;
OS Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia; Sciurognathia;
Muridae; Murinae; Mus.
NCBI TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=99279233; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RA Kawai J., Shinsagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Furukuda S.,
Aizawa K., Izakawa M., Nishio K., Kiyobono H., Kondo S., Yamamoto I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadora K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh R.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincic S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Monbaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seiya T., Storch K.-P.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=22354633; PubMed=12466693; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Yagi K., Tomaru Y., Hasegawa Y., Hume A., Schonbach C., Gojobori T.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Blake J.A., Dragni T.A., Fletcher C.C., Forrest C.E., Cousins S.,
Dalla E., Dragni T.A., Fletcher C.C., Frazer K.S.,
Ra Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
Grindmond S., Gustincic S., Hirokawa N., Jackson J.I., Jarvis E.D.,
Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Nagashima T., Numata K., Okido T., Pavon W.J., Perete G., Pesole G.,
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
- Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yamagishi M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsuka N., Hironae Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Akizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
RN [4]
RP "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hirao T., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Kashiwagi K., Fujikawa S., Inoue K., Togawa Y., Iwasa M., Ohara E., Watanuki M., Yonega Y., Ishikawa T., Ozawa K., Tanaka T., Matsubara S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system 3.84-format sequencing pipeline with 384 multicapillary sequencer.";
RL Genomics Res. 10:1757-1771 (2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hirao T., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Kashiwagi K., Katcho H., Kawei J., Koizima T., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Obata N., Okazaki Y., Saito R., Saitoh H., Saito K., Sakai K., Sakazume N., Sano H., Sasaki D., Shiba K., Shingawa A., Shiraki T., Sogabe Y., Tagami M., Tagava A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL 2001) to the RIBI/EMBL/GenBank/DBJ databases.
DR EMBL; AK051592; BAC34684.1; -; mRNA.
DR MGII; MGI:109349; AfC2.
DR GO; GO:00036777; P:DNA binding; IDA.
DR GO; GO:0005515; P:protein binding; IPI.
KW DNA-binding; Nuclear protein.
SQ SEQUENCE 447 AA; 48002 MW; 35A0751C1627D682 CRC64;
Query Match 57.3%; Score 445; DB 2; Length 447;
Best Local Similarity 70.1%; Pred. No. 2, 9e-27;
Matches 103; Conservative 1; Mismatches 29; Indels 14; Gaps 4;
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Db 5 WWWPDQTPTFLNKCEYGLFNPLASPPNEPKASEDIKHNPLDSPLATPIRSK 64
Qy 63 IEEPSVVEETHQDSSLPHPSSTSDEKEYPLACTAQPTSAVRPASQVNLLTSQDSS 122
Db 65 IEEPSVVEETHQDSSLPHPSSTSDEKEYPLACTAQPTSAVRPASQVNLLTSQDSS 124
Qy 123 VIIQQAAPSPSSTVTQAFSSNRIV 149
Db 125 VIIQQAAPSPSSTVTQAFSSNRIV 151

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AC				Db	121	RPHESITSDKEVKPLAQTAQTSAYTBRASIQVNNTLSSDSVVIQQAVPSPTS	150
DT 25-OCT-2004	(TREMBrel. 28, Created)						
DT 25-OCT-2004	(TREMBrel. 28, Last sequence update)						
DT 25-OCT-2004	(TREMBrel. 28, Last annotation update)						
DE AT52 protein.							
GN Name=Atf2;							
OS Mus musculus (Mouse).							
OC Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;							
OC Muridae; Murinae; Mus.							
OX NCBI_TAXID=10990;							
RN [1]							
RP NUCLEOTIDE SEQUENCE [DNA].							
RC STRAIN=C57BL/6; TISSUE-Head.							
RX MEDLINEB22388257; Published=1477932; DOI=10.1073/pnas.242603899;							
RA Strausberg R.L., Feingold E.A., Grouse L.H., Grouse L.H., Derge J.G.,							
RA Klausner R.D., Collins F.S., Wagner L., Schuler G.D., Schuler G.D.,							
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Schaefer C.F.,							
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Bhat N.K.,							
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,							
RA Stoeckert M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Scheetz T.E.,							
RA Brownstein M.J., Usdin T.B., Tohjiyuki S., Carninci P., Prange C., Prange C.,							
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullally S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullally S.J.,							
RA Bosak S.A., McBryan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Bosak S.A., McBryan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,							
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,							
RA Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,							
RA Fahey J., Heitton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Fahey J., Heitton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,							
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,							
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,							
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Grimwood J., Schmutz J., Myers R.M.,							
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialus D.E.,							
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., RT Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences." RT							
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).							
RN [2]							
RP NUCLEOTIDE SEQUENCE [DNA].							
RC STRAIN=C57BL/6; TISSUE-Head.							
RA Director MGC Project;							
DR Submitted (SEPB-2004) to the EMBL/GenBank/DDBJ databases.							
DR EMBL; BC082596; AAH82596..1; -; mRNA.							
DR SRR; Q640L6..238-298.							
DR MG1; MG1:109349; Atf2.							
DR GO; GO:0003677; F-DNA binding; IDA.							
DR GO; GO:0005515; P:protein binding; IPF.							
DR InterPro; IPR011616; bZIP 1.							
DR InterPro; IPR000837; LeuZip_Fos.							
DR InterPro; IPR04877; TF_bZIP.							
DR InterPro; IPR007071; znf_C2H2.							
DR Pfam; PF00096; zf_C2H2_1.							
DR Pfam; PF00042; LBU21PFRFG.							
DR SMART; SM00318; BLU2_1.							
DR PROSITE; PS55217; BZIP_1.							
DR PROSITE; PS00036; BZIP_BASIC_1.							
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.							
DR PROSITE; PS55157; ZINC_FINGER_C2H2_2; UNKNOWN_1.							
DR SEQUENCE 389 AA; 42345 MW; 770AD65BA6114F10 CRC64;							
Query Match Score 366; DB 2; Length 369;							
Best Local Similarity 45.5%; Pred. No. 4.8e-21; Indels 86; Gaps 4;							
Matches 80; Conservative 6; Mismatches 4;							
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Db 1 MSDDKPFLCTAPGGCQRFTNEDHLAVHKHEMLKFGPARNDSVIVADQTQPPTRFLKN							
Qy 61 -----SKIEEPSSVETTHODSPL 78							

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OM protein - protein search, using sw model

Run on: January 10, 2006, 23:02:23 ; Search time 23 Seconds
(without alignments)

535.595 Million cell updates/sec

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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73.6	94.8	501	2 US-09-549-016-11281	Sequence 11281, A
2	21.2	27.3	502	2 US-09-513-999C-7023	Sequence 7023, Ap
3	13.7	17.7	29	2 US-09-503-954A-20	Sequence 20, Appli
4	13.7	17.5	29	2 US-09-515A-20	Sequence 6, Appli
5	11.5	14.8	27	2 US-08-819-177-6	Sequence 11, Appli
6	10.9	14.0	447	2 US-09-334-332-11	Sequence 15, Appli
7	10.6	5.5	97	2 US-09-395-448-15	Sequence 15, Appli
8	10.6	5.5	97	2 US-09-796-15	Sequence 15, Appli
9	10.6	5.5	97	2 US-09-341-450-15	Sequence 15, Appli
10	10.3	13.3	522	2 US-09-349-016-11145	Sequence 11145, A
11	10.2	13.2	496	1 US-08-224-482-2	Sequence 2, Appli
12	10.2	13.2	533	1 US-08-040-548-1	Sequence 1, Appli
13	10.2	13.2	533	1 US-08-466-344-1	Sequence 21, Appli
14	10.2	13.2	533	2 US-09-546-013-21	Patent No. 5200152
15	10.2	13.2	533	6 5.06152-2	Sequence 108, Appli
16	10.2	13.2	1367	2 US-09-487-558B-108	Sequence 2, Appli
17	10.2	13.1	409	2 US-09-029-755C-2	Sequence 42, Appli
18	10.2	13.1	443	2 US-09-942-335C-42	Sequence 42, Appli
19	10.2	13.1	443	2 US-09-244-367-42	Sequence 42, Appli
20	10.0	12.9	383	2 US-09-248-756A-19589	Sequence 19589, A
21	9.8	12.7	380	2 US-09-248-756A-19662	Sequence 19662, A
22	9.7	12.6	94	2 US-09-329-007A-9	Sequence 9, Appli
23	9.7	12.6	94	2 US-10-113-424-9	Sequence 9, Appli
24	97.5	12.6	94	2 US-09-716-637-16	Sequence 16, Appli
25	97.5	12.6	168	1 US-09-553-476-73	Sequence 73, Appli
26	97.5	12.6	176	1 US-09-348-776A-18892	Sequence 18892, A
27	97.5	12.6	241	1 US-08-353-476-116	Sequence 116, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-11281
; Sequence 11281, Application US/09949016
; Patent No. 6812319
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09-349,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSSQ for Windows Version 4.0
; SEQ ID NO: 11281
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11281

Query Match 94.8%; Score 736; DB 2; Length 501;
Best Local Similarity 71.3%; Pred. No. 4.3e-11;
Matches 149; Conservative Matches 149; Indels 60; Gaps 1;

Qy 1 MKFLKLVNSARQYDLDWNSDDKPPLECTAGPGQRFNTEDHLAVTKHKGHEMTLKGCPARN 60
Db 5 MKFLKLVNSARQYDLDWNSDDKPPLECTAGPGQRFNTEDHLAVTKHKGHEMTLKGCPARN 64
61 ----- 60

Qy 65 DSIVADQTPPTPLKNCBEGVLNTELASPFFENKKASEDDIKMPDLISPLATPIIR 124
Db 61 SKIBBSVVETTHQSPPLPHPESTSDEKEVPLAQTAQPSAIVRASLOVNPVNLITSSD 120
Qy 125 SKIBBSVVETTHQSPPLPHPESTSDEKEVPLAQTAQPSAIVRASLOVNPVNLITSSD 184
Db 121 SSVIQQAVSPTSSVTQAPSNSRPIV 149
Qy 185 SSVIQQAVSPTSSVTQAPSNSRPIV 213
; RESULT 2
US-09-513-999C-7023
; Sequence 73, Application US/09513999C
; Patent No. 6783961

GENERAL INFORMATION:
 / APPLICANT: Dumas Milne Edwards, J.B.
 / APPLICANT: Duclert, A.
 / APPLICANT: Giordano, J.Y.
 / TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 / Patent No. 67839561
 / FILE REFERENCE: 59.US2.REG
 / CURRENT FILING DATE: 2000-02-04
 / PRIOR APPLICATION NUMBER: US/09/513, 993C
 / PRIOR FILING DATE: 1999-02-26
 / NUMBER OF SEQ ID NOS: 36681
 / SOFTWARE: Patentin.pml
 / SEQ ID NO 7023
 / LENGTH: 52
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: UNSURE
 / LOCATION: 6
 / OTHER INFORMATION: Xaa=Pro or Ser
 US-09-513-993C-7023

Query Match 27 3%; Score 212; DB 2; Length 52;
 Best Local Similarity 80.0%; Pred. No. 8.7e-16;
 Matches 36; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

RESULT 3
 US-09-503-954A-20
 / Sequence 20. Application US/09503954A
 / Patent No. 6610820
 / GENERAL INFORMATION:
 / APPLICANT: Bonny, Christophe
 / TITLE OF INVENTION: CELL-PERMEABLE PEPTIDE INHIBITORS OF THE JNK SIGNAL
 / FILE REFERENCE: 20349-501
 / CURRENT APPLICATION NUMBER: US/09/503, 954A
 / CURRENT FILING DATE: 2000-02-14
 / PRIOR APPLICATION NUMBER: US/99 60/158, 774
 / PRIOR FILING DATE: 1999-10-12
 / NUMBER OF SEQ ID NOS: 20
 / SOFTWARE: Patentin Ver. 2.0
 / SEQ ID NO 20
 / LENGTH: 29
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: chemically synthesized

Query Match 17.7%; Score 137; DB 2; Length 29;
 Best Local Similarity 88.9%; Pred. No. 5e-08;
 Matches 24; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 4
 US-09-970-515A-20
 / Sequence 20. Application US/09970515A
 / Patent No. 6780970
 / GENERAL INFORMATION:
 / APPLICANT: Bonny, Christophe
 / TITLE OF INVENTION: CELL-PERMEABLE PEPTIDE INHIBITORS OF THE JNK SIGNAL
 / FILE REFERENCE: 20349-501 DIV

CURRENT APPLICATION NUMBER: US/09/970, 515A
 / CURRENT FILING DATE: 2001-10-03
 / PRIOR APPLICATION NUMBER: 09/503, 954
 / PRIOR FILING DATE: 2000-02-14
 / PRIOR APPLICATION NUMBER: 60/158, 774
 / PRIOR FILING DATE: 1999-10-12
 / NUMBER OF SEQ ID NOS: 21
 / SOFTWARE: Patentin Ver. 2.0
 / SEQ ID NO 20
 / LENGTH: 29
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: chemically synthesized

Query Match 17.7%; Score 137; DB 2; Length 29;
 Best Local Similarity 88.9%; Pred. No. 5e-08;
 Matches 24; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 5
 US-08-819-177-6
 / Sequence 6. Application US/08819177
 / Patent No. 6043083
 / GENERAL INFORMATION:
 / APPLICANT: Davis, Roger J.
 / APPLICANT: Dickens, Martin
 / TITLE OF INVENTION: INHIBITORS OF THE JNK SIGNAL
 / NUMBER OF SEQUENCES: 30
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Fish & Richardson, P.C.
 / STREET: 225 Franklin Street
 / CITY: Boston
 / STATE: MA
 / COUNTRY: US
 / ZIP: 02110-2804
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: Windows 95
 / SOFTWARE: FastSEQ for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/819,177
 / FILING DATE: 28 April 1997
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER:
 / FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Fasse, J. Peter
 / REGISTRATION NUMBER: 32,983
 / REFERENCE/DOCKET NUMBER: 07917/037001
 / TELEPHONE: 617-542-5070
 / TELEFAX: 617-542-8906
 / INFORMATION FOR SEQ ID NO: 6:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 27 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: peptide
 / FEATURE:
 / OTHER INFORMATION: ATF-2 JNK-binding domain

Query Match 14.8%; Score 115; DB 2; Length 27;
 Best Local Similarity 87.0%; Pred. No. 1.1e-05;
 Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

US-08-819-177-6

RESULT 6
 Qy 41 HLAHKHKGMLKFGPARNSKI 63
 Db 1 HLAHKHKGMLKFGPARNDSV 23
 ; Sequence 11; Application US/09234332A
 ; Patent No. 6087158
 ; GENERAL INFORMATION:
 ; APPLICANT: Cedars-Sinai Medical Center
 ; APPLICANT: Michel F. Levesque, M.D.
 ; TITLE OF INVENTION: CONVERSION OF NON-NEURONAL CELLS INTO NEURONS; TRANSDIFFERENTIATION OF EPIDERMAL CELLS
 ; FILE REFERENCE: P07 41494
 ; CURRENT APPLICATION NUMBER: US/09/234,332A
 ; CURRENT FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastS2Q for Windows Version 3.0
 ; SEQ ID NO: 11
 ; LENGTH: 447
 ; TYPE: PRT
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (0) ..(0)
 ; OTHER INFORMATION: Zic 1 protein; Genbank Accession D76435.
 US-09-234-332-11

Query Match 14.0%; Score 109; DB 2; Length 447;
 Best Local Similarity 26.1%; Pred. No. 0.0024;
 Matches 42; Conservative 25; Mismatches 58; Indels 36; Gaps 7;
 SEQ ID NO: 15

Qy 2 KFKLHVNSARQYKDLWNMSDDKKPFLCTAPCGQFTNEDHLAVHKHKGMLKFGP--- 57
 Db 286 KYKL-VNHRVH----IGEKPPFPCCPKCFFEG 338
 US-09-234-332-11

Query Match 14.0%; Score 109; DB 2; Length 447;
 Best Local Similarity 26.1%; Pred. No. 0.0024;
 Matches 42; Conservative 25; Mismatches 58; Indels 36; Gaps 7;
 SEQ ID NO: 15

Qy 58 ----ARNSKIEEFSVVEFHQ-----DSDLPHPESTSDER-EVPLAQTIQOPTSAV 104
 Db 339 CDRRFANSRDKKEMAHVHTSDKPKYLCKMCKSYRHKMVHESSQGSQSPA-- 396
 US-09-234-332-11

Query Match 14.0%; Score 109; DB 2; Length 447;
 Best Local Similarity 26.1%; Pred. No. 0.0024;
 Matches 42; Conservative 25; Mismatches 58; Indels 36; Gaps 7;
 SEQ ID NO: 15

Db 397 -----ASSGYESSSTPPTIVSPSTDNPITSSL---SPSSS 427
 US-09-234-332-11

RESULT 7
 Qy 17 WNMSSDKPFLCTAPCGQFTNEDHLAVHKHKGMLKFG---PARNSKIEEFSVVERT 72
 Db 31 WH-TGERPPFMCTNSYCGKRPFTNRDTLARKRTRTGEKCPACPCPKFMRSDHLSKHKT 89
 ; Sequence 15; Application US/09925796
 ; Patent No. 6777185
 ; GENERAL INFORMATION:
 ; APPLICANT: Case, Casey C.
 ; APPLICANT: Zhang, Lei
 ; TITLE OF INVENTION: Functional Genomics Using Zinc Finger Proteins
 ; FILE REFERENCE: 019496-002000US
 ; CURRENT APPLICATION NUMBER: US/09/925,796
 ; CURRENT FILING DATE: 2001-08-09
 ; PRIORITY NUMBER: 09/395,448
 ; PRIORITY FILING DATE: 1999-09-14
 ; PRIORITY NUMBER: 09/229,037
 ; PRIORITY FILING DATE: 1999-01-12
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 15

Query Match 13.7%; Score 106.5; DB 2; Length 97;
 Best Local Similarity 39.7%; Pred. No. 0.00053;
 Matches 25; Conservative 9; Mismatches 24; Indels 5; Gaps 2;
 SEQ ID NO: 15

Qy 17 WNMSSDKPFLCTAPCGQFTNEDHLAVHKHKGMLKFG---PARNSKIEEFSVVERT 72
 Db 31 WH-TGERPPFMCTNSYCGKRPFTNRDTLARKRTRTGEKCPACPCPKFMRSDHLSKHKT 89
 ; Sequence 15; Application US/09941450
 ; Patent No. 6780590
 ; GENERAL INFORMATION:
 ; APPLICANT: Case, Casey C.
 ; APPLICANT: Urtnov, Fyodor
 ; TITLE OF INVENTION: Functional Genomics Using Zinc Finger Proteins
 ; FILE REFERENCE: 019496-002000US
 ; CURRENT APPLICATION NUMBER: 8325-0007.20
 ; CURRENT FILING DATE: 2001-08-28
 ; PRIORITY NUMBER: US/09/941,450
 ; PRIORITY FILING DATE: 1999-09-14
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 15

Query Match 13.7%; Score 106.5; DB 2; Length 97;
 Best Local Similarity 39.7%; Pred. No. 0.00053;
 Matches 25; Conservative 9; Mismatches 24; Indels 5; Gaps 2;
 SEQ ID NO: 15

Qy 17 WNMSSDKPFLCTAPCGQFTNEDHLAVHKHKGMLKFG---PARNSKIEEFSVVERT 72
 Db 31 WH-TGERPPFMCTNSYCGKRPFTNRDTLARKRTRTGEKCPACPCPKFMRSDHLSKHKT 89
 ; Sequence 15; Application US/09395448
 ; Patent No. 6595992
 ; GENERAL INFORMATION:
 ; APPLICANT: Case, Casey C.
 ; APPLICANT: Zhang, Lei
 ; APPLICANT: Sangamo Biosciences, Inc.
 ; TITLE OF INVENTION: Functional Genomics Using Zinc Finger Proteins
 ; FILE REFERENCE: 019496-002000US
 ; CURRENT APPLICATION NUMBER: US/09/395,448
 ; CURRENT FILING DATE: 1999-09-14
 ; PRIORITY NUMBER: 09/229,007
 ; PRIORITY FILING DATE: 1999-01-12
 ; PRIORITY NUMBER: 09/229,037
 ; PRIORITY FILING DATE: 1999-01-12
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.1
 ; LENGTH: 97
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Description of Artificial Sequence:designed ZFP
 US-09-395-448-15

OTHER INFORMATION: Description of Artificial Sequence:designed ZFP
 US-09-941-450-15

Query Match Similarity 13.7%; Score 106.5; DB 2; Length 97;
 Best Local Similarity 39.7%; Pred. No. 0.00053;
 Matches 25; Conservative 9; Mismatches 24; Indels 5; Gaps 2;

Qy 17 WNSDDKPKFLCTAPGCGQRFTNEDHLAVHKhKHETLKF|----PARNSKIEBPSVWETT 72
 Db 31 WH-TGERPFCMTCIWSYCGKRFTRNDTLARHKhRTHTGEKKFACPECPKRFMERSDHLSKhXT 89

Qy 73 HQD 75
 Db 90 HQN 92

RESULT 10
 US-09-949-016-11145
 ; Sequence 11145, Application US/09949016
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 11145
 ; LENGTH: 522
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-11145

Query Match Similarity 13.3%; Score 103; DB 2; Length 522;
 Best Local Similarity 25.7%; Pred. No. 0.013; Mismatches 18; Indels 63; Gaps 8;
 Matches 44

Qy 9 SARQYDWM-SDDRPFLCTAPGCGQRFTNED---HLAVHKh-----KHEMT 52
 Db 305 SATNYKHNVRHTGEKPYCIVPGCGRFRTESSLYKHHVHTHCKPYTCTGKTYRQT 364

Qy 53 LKFGPARNSKIEBPSVWETTQ-----DSPLP-HPE----STSDEKEVP 92
 Db 365 STLMHKRSAGBLETTEESEQALYBQQQLEEASAEESSPPKRPIAYLSEVKERDDI 424

Qy 93 LAQTAQTSATVTPASLQPVNPYLTSDDSVIQQAVPSSTSSTVQAPS 143
 Db 425 PAQAVMVE----EDGAPQVALITDGA---QQTITSGAVVAEDSS 465

RESULT 11
 US-08-224-482-2
 ; Sequence 2, Application US/08224482
 ; GENERAL INFORMATION:
 ; APPLICANT: Mercola, Dan
 ; Patent No. 5831692
 ; TITLE OF INVENTION: Inhibition of the Mitogenic Activity of
 ; TITLE OF INVENTION: PDGF by Mammalian EGFR
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell and Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California

COUNTRY: USA
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/224,482
 FILING DATE: 07-APR-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-ME 9913
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 496 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-224-482-2

Query Match Similarity 13.2%; Score 102.5; DB 1; Length 496;
 Best Local Similarity 26.7%; Pred. No. 0.014;
 Matches 35; Conservative 22; Mismatches 51; Indels 23; Gaps 5;

Qy 22 DKPPLCTAPGCGQRFTNED-----HLAVHKhHEMTLKFGPARNSKIEBPSVWETT 73
 Db 354 EKPFACDI--CGRKARSDERKHTKHLRQDKDADKSKVVASPAASSLSSYPSPATSY 411

Qy 74 QDSPLPHPESTSDKEVPLAQTAAQTSALVTPASLQPVNPYLTSDDSVIQQAVPSPT 133
 Db 412 ----PSP-ATTSPSPVPPTSYYSSPGSSTYSPSPAHGFPSPSVAITFASV-----PPA 458

Qy 134 SSTVTTQAPSS 144
 Db 459 FPTQVSFPSSA 464

RESULT 12
 US-08-040-548-1
 ; Sequence 1, Application US/08040548
 ; Patent No. 5763209
 ; GENERAL INFORMATION:
 ; APPLICANT: Subhatne, Vikas P.
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
 ; FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
 ; NUMBER OF SEQUENCES: 67
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: 321 No. 5763209th Clark Street, Suite 800
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60610
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.1, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/040,548
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Coughlin, Daniel F.
 REGISTRATION NUMBER: 36,111
 REFERENCE/DOCKET NUMBER: arcd067
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 744-0090
 TELEFAX: (312) 245-4961
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 533 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-040-548-1

Query Match 13.2%; Score 102.5; DB 1; Length 533;
 Best Local Similarity 26.7%; Pred. No. 0.016;
 Matches 35; Conservative 22; Mismatches 51; Indels 23; Gaps 5;

Qy 22 DKPFLCTAAGCGQRFNTED-----HLAVHGHKHEMTLKGPARNSKIEEPSVETTH 73
 Db 391 EKPPACDI--CGRKPARSDRKRTKIHARQDKCKADSKVVASPAASSLSSYSPVATSY 448

Qy 74 QDSDLPHPESTSDEKEVPLAQTAOPTSAIVRASLQVPNVLTSQSSVIIQQAVPSPT 133
 Db 449 ----PSP-ATTSPSPVPTSYSSPGSSTYSPSPAHSGFPSPSVATTFFASV-----PPA 495

Qy 134 SSTVITQAPSS 144
 Db 496 FPTQVSSFPFA 506

RESULT 13
 US-08-466-344-1
 Sequence 1, Application US/08466344
 GENERAL INFORMATION:
 APPLICANT: Sukhatme, Vikas P.
 TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
 NUMBER OF SEQUENCES: 67
 ADDRESSEE: Arnold, White & Durkee
 STREET: 321 No. 5775583th Clark Street, Suite 800
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60610
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/466-344
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/040, 548
 FILING DATE: 31-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Coughlin, Daniel F.
 REGISTRATION NUMBER: 36,111
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 744-0090
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 533 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-466-344-1

Query Match 13.2%; Score 102.5; DB 1; Length 533;

Best Local Similarity 26.7%; Pred. No. 0.016; Matches 35; Conservative 22; Mismatches 51; Indels 23; Gaps 5;

Qy 22 DKPFLCTAAGCGQRFNTED-----HLAVHGHKHEMTLKGPARNSKIEEPSVETTH 73
 Db 391 EKPPACDI--CGRKPARSDRKRTKIHARQDKCKADSKVVASPAASSLSSYSPVATSY 448

Qy 74 QDSDLPHPESTSDEKEVPLAQTAOPTSAIVRASLQVPNVLTSQSSVIIQQAVPSPT 133
 Db 449 ----PSP-ATTSPSPVPTSYSSPGSSTYSPSPAHSGFPSPSVATTFFASV-----PPA 495

Qy 134 SSTVITQAPSS 144
 Db 496 FPTQVSSFPFA 506

RESULT 14
 US-09-546-013-21
 Sequence 21, Application US/09546013
 GENERAL INFORMATION:
 APPLICANT: Yuan, Chong-Shen
 TITLE OF INVENTION: METHODS FOR ASSAYING S-ADENOSYL METHIONINE-DEPENDENT Methyltransferase
 FILE REFERENCE: 10937-1652
 CURRENT APPLICATION NUMBER: US/09/546, 013
 CURRENT FILING DATE: 2000-04-10
 EARLIER APPLICATION NUMBER: 09/347, 878
 EARLIER FILING DATE: 1999-07-06
 EARLIER APPLICATION NUMBER: 09/457, 205
 NUMBER OF SEQ ID NOS: 94
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 21
 LENGTH: 533
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Human Egr Dna binding protein: zinc finger domain
 PUBLICATION INFORMATION:
 PATENT DOCUMENT NUMBER: 5,866,325
 PATENT FILING DATE: 1995-06-06
 PUBLICATION DATE: 1999-02-02
 US-09-546-013-21

Query Match 13.2%; Score 102.5; DB 2; Length 533;
 Best Local Similarity 26.7%; Pred. No. 0.016; Matches 35; Conservative 22; Mismatches 51; Indels 23; Gaps 5;

Qy 22 DKPFLCTAAGCGQRFNTED-----HLAVHGHKHEMTLKGPARNSKIEEPSVETTH 73
 Db 391 EKPPACDI--CGRKPARSDRKRTKIHARQDKCKADSKVVASPAASSLSSYSPVATSY 448

Qy 74 QDSDLPHPESTSDEKEVPLAQTAOPTSAIVRASLQVPNVLTSQSSVIIQQAVPSPT 133
 Db 449 ----PSP-ATTSPSPVPTSYSSPGSSTYSPSPAHSGFPSPSVATTFFASV-----PPA 495

Qy 134 SSTVITQAPSS 144
 Db 496 FPTQVSSFPFA 506

RESULT 15
 5206152-2
 ; Patent No. 5206152
 ; APPLICANT: SUKHATME, VIKAS P.
 ; TITLE OF INVENTION: CLONING AND EXPRESSION OF EARLY GROWTH
 ; REGULATORY PROTEIN GENES
 ; NUMBER OF SEQUENCES: 18
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/249, 584
 ; FILING DATE: 26-SEP-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 179, 587

i FILING DATE: 08-APR-1988
;SEQ ID NO:2:
; LENGTH: 533
5206152-2

Query Match 13.2%; Score 102.5; DB 6; Length 533;
Best Local Similarity 26.7%; Pred. No. 0.016;
Matches 35; Conservative 22; Mismatches 51; Indels 23; Gaps 5;

Qy 22 DKPFLCTAPGGCGRTFNE-----HLAVIHKHHEMTLKGPARNSKIEBPSVVFTH 73
Db 391 EKPFACDI-CGRKFARSDERKRHTKIHRLQDKADKSVVASPAASSLSSYSPVATSY 448

Qy 74 QDSPLPHPESTSDEKEVPLAOTAQPTSAIVRPAQLQPVNLTSSDSSVVIQQAVPSPR 133
Db 449 ----PSP-ATISFPSPVPTTSSPGSSTPSPAHSGFSPSPSVAITFASV-----PPA 495

Qy 134 SSTVITQAPSS 144
Db 496 FTQVSSFPFA 506

Search completed: January 10, 2006, 23:07:30
Job time : 24 sec's

Copyright (c) 1993 - 2006 Compugen Ltd.	GenCore version 5.1.6	AF483482	Mus muscu
OM protein - nucleic search, Using frame_plus_p2n.model		AF483483	Mus muscu
Run on: January 12, 2006, 17:52:40 ; (without alignments)	search time 3044 Seconds	U16159	Xenopus lae
Title: AAH26175_COPY_50_65	298.783 Million cell updates/sec	S76657	cyclic AMP
Perfect score: 81	emtlkfpgarnskie 16	AX821940	Sequence
Sequence: DeIop	6.0 , DeIext 7.0	AX822000	Sequence
Scoring table: BLOSUM62	Xgapext 10.0 , Xgapext 0.5	X15875	Human mRNA
	Ygapop 10.0 , Ygapext 0.5	BC026175	Homo sapi
	Fgapop 6.0 , Fgapext 7.0	DQ003047	Homo sapi
	DeIop 6.0 , DeIext 7.0	Y17724	Gallus galli
Searched: 5883141 seqs, 28421725653 residues		QQ003049	Homo sapi
Total number of hits satisfying chosen parameters: 11766282		DQ003049	Rattus norv
Minimum DB seq length: 0		DQ003049	Macaca fa
Maximum DB seq length: 2000000000		AB169461	Macaca fa
Post-processing: Minimum Match 0%	Maximum Match 100%	DQ003049	Homo sapi
	Listing first 45 summaries	DQ003049	Homo sapi
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-Q=cgn2_1/USPOOL_SPOOL_RAWLINGS10076905/runat_10012006_144223_5320/app_query.fasta_1.199		AC074291	Homo sapi
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-UNITS-bits -START=1 -END=1 -MATRIX=blossum62 -TRANS=human40.cdi -LIST=45		AC19682	Rattus no
-DOALIGN=200 -NORM=ext -HEAPSIZE=5000 -MINLEN=0 -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL		AC129355	Rattus no
-OUTFMT=ofo -NORM=ext -HEAPSIZE=5000 -MINLEN=0 -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL		AC161794	Homo sapi
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-DEV TIMEOUT=120 -WARN 1 -THREADES=1 -XGAPPOP=1.0 -XGAPEXT=0.5 -FGAPPOP=6		AX32119	Sequence
-FGAPTEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7		BD026693	Sequence
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2: gb_ln:*		CO491274	Sequence
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7: gb_bh:*		CO491274	Sequence
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9: gb_ro:*		CO491274	Sequence
10: gb_sts:*		CO491274	Sequence
11: gb_by:*		CO491274	Sequence
12: gb_un:*		CO491274	Sequence
13: gb_vj:*		CO491274	Sequence
14: gb_htg:*		CO491274	Sequence
15: gb_pl:*		CO491274	Sequence
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES			
Result No.	Score	Query Length	DB ID
1	61	75.3	1209 9 RATRATF2
2	61	75.3	1302 9 S76659
3	61	75.3	1370 8 EC026175

ALIGNMENTS			
RESULT 1	RATRATF2	1209 bp	
LOCUS	RAT RATF2 mRNA, complete cds.		
DEFINITION			
ACCESSION	M65148		
VERSION	GI:206569		
KEYWORDS			
ORGANISM	Rattus norvegicus (Norway rat)		
SOURCE	Battus norvegicus Mammalia; Eutheria; Buarchoontoliens; Glires; Murinae; Rattus.		
REFERENCE	Sciurognathi; Murioidea; Metacota; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Kageyama,R., Sasai,Y. and Nakanishi,S.		
TITLE	Molecular characterization of transcription factors that bind to the cAMP responsive region of the substance P precursor gene. CDNA cloning of a novel C/EBP-related factor		
JOURNAL	J. Biol. Chem. 266 (23), 15525-15531 (1991)		
PUBMED	1714459		
COMMENT	Original source text: Rat, cDNA to mRNA.		
FEATURES	Location/Qualifiers		
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	organism="Rattus norvegicus"		
	/mol_type="mRNA"		
	/strain="Sprague-Dawley"		
	/db_xref="taxon:10116"		
	/dev_stage="adult"		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	61	75.3
3	61	75.3

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S76659 cyclic AMP
EC026175 Homo sapi

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		Percent Similarity:	85.71%
		Best Local Similarity:	78.57%
		Query Match:	75.31%
		DB:	9
		Mismatches:	2
		Indels:	0
		Gaps:	0
		Query	AAH26175_COPY_50_65 (1-16) x S76659 (1-1302)
		Db	185 GAGATGACACTGAATTGGTCAGCACGTTAATGACAGTGTIC 226
		RESULT 3	
		LOCUS	BC026175
		DEFINITION	Homo sapiens activating transcription factor 2, mRNA (cDNA clone IMAGE:410809), complete cds.
		ACCESSION	BC026175
		VERSION	BC026175.1 GI:20072896
		KEYWORDS	
		SOURCE	Homo sapiens (human)
		ORGANISM	Homo sapiens
		MATERIALS	Bukaryota; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo
		REFERENCE	1 (bases 1 to 1370)
		AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Schuler, G.D., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altachuri, S.F., Zeeberg, B.R., Buetow, K.H., Schaefer, C.P., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Marx, S.I., Wang, J.J., Heisler, F., Diatchenko, L., Marusina, K., Farmer, A.R., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshinuki, S., Carninci, P., Prange, C., Raha, S.A., Locquelet, N.A., Peters, G.J., Abramson, R.D., Mulahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Murry, D.M., Sodergren, E.J., Lu X., Gibbs, R.A., Fahay, J., Helton, B., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smialus, D.E., Schnurch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
		VERSION	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
		TITLE	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
		JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
		PURMED	12477932
		REFERENCE	2 (bases 1 to 1370)
		AUTHORS	Strausberg, R.
		TITLE	Direct Submission (02-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
		JOURNAL	NIH-MGC Project URL: http://mgc.nci.nih.gov
		PUBLISHED	Contact: MGC help desk Email: csgaps-r@mail.nih.gov
		REMARK	Tissue Procurement: ATCC/DCD/DTP
		COMMENT	CDNA Library Preparation: CLONTECH Laboratories, Inc.
			CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LJNLN)
			DNA Sequencing by: Institute for Systems Biology
			http://www.systemsbiology.org
			contact: amadan@systemsbiology.org
			Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whitting
FEATURES		ORGANISM	
source		MUS sp.	
		Mammalia; Chordata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;	
		Sciurognathii; Muridae; Murinae; Mus.	
		REFERENCE	
		AUTHORS	Georgopoulos, K., Morgan, B.A. and Moore, D.D.
		TITLE	Functionally distinct isoforms of the CRE-BP DNA-binding protein mediates activity of a T-cell specific enhancer
		JOURNAL	Mol. Cell. Biol. 12 (2), 747-757 (1992)
		PUBLISHED	1531087
		REMARK	GenBank entry [NCBI] Gribbsq_76659 from the original journal article.
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		/db_xref="GI:241431"	
		/translation="MTLKFGPARNLDSLPLATPIIIRSKIEPSVYETTHQDPLPHPESTISDEKLVR EFKKASEDDIKMPMLDLSPLATPIIIRSKIEPSVYETTHQDPLPHPESTISDEKLVR PVTMVSPVGIFGPSSQPOYEAOKRLAQTQHPPTVKGHGSGLVQSE ESPPQSLQQPATSTTEPASPAHTRTPTOTNSGRERAANEDPEDEKRKLERNRAAA SCRQKRKRVWYQSVLEKAEDLSLNGQLOSEVTLRNEAQKQLLAKHDPCPTAMQ	

/db_xref="GI 19548720"	
/translation="MSDDCKPFLCTAGCCQRFFINEDHLAVKHKHEMLKFGPARND	
VIVADOTENPTPLKNCNEVGFLNELASPFKKASEDDIKMPIDLSPLATPIR	
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SDSVEVIIQAVPAPPTTSITOPVTPGSSPVGQPPVTPGSSPVOVOSAKMRKAALCOHPPNTGDT	
VICHGSGLVRTOESRPSLQDQPATSTETTASPAHTPTQONTSGRRRAANEDPD	
EKRKFLLRNRAASRCRKTKWQSLKDKDLSSINGQLOSEVTLRNEVAQLQ	
LJIAHKDOPVTAMOKSGEYHTAOKDSDSEEDLSPPSSPTEAICHSYSVTNSGVSSTSK	
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PRIGGIN	
Alignment Scores:	
Pred. No.: 0.0356	Length: 1464
Score: 61.00	Matches: 11
Arcent. Similarity: 85.71%	Conservative: 1
Arcent. Local Similarity: 78.57%	Mismatches: 0
Query Match: 75.31%	Indels: 0
9:	Gaps: 0
AAH26175_COPY_50_65 (1-16) x AF4831483 (1-1464)	
/	1 GluMetThrLeuLysPheGlyProAlaArgSerLysIle 14
/	94 GAGGTGACACTGAATTGGTCAGCAGTAATGACAGTGTCTC 135
RESULT 6	
U16158	XIUI16158 1520 bp mRNA activating transcription factor 2 (ATF2) mRNA, Xenopus laevis
DEFINITION	complete cds.
ACCESSION	U16158
ORGANISM	Xenopus laevis (African clawed frog)
KEYWORDS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.
REFERENCE	1 (bases 1 to 1520)
AUTHORS	Villarreal, X. C. and Richter, J. D.
TITLE	Analysis of ATF2 gene expression during early Xenopus laevis development
JOURNAL	Gene 153 (2), 225-229 (1995)
REFERENCE	2 (bases 1 to 1520)
AUTHORS	Richter, J. D.
TITLE	Direct Submission
JOURNAL	Submitted (20-OCT-1994) Joel D. Richter, Worcester Foundation for Experimental Biology 222 Maple Avenue, Shrewsbury, MA 01545, USA
COMMENT	On Jul 6, 1995 this sequence version replaced gi:710325.
FEATURES	
source	1..1520
/organism="Xenopus laevis"	
/mol_type="mRNA"	
/db_xref="taxon:8355"	
/clone="PATF2"	
/cell_type="oocyte"	
1..1520	
gene	
/gene="ATF2"	
CDS	
/gene="ATF2"	
/codon_start=1	
/evidence="experimental transcrip	
/product="activating transcrip	
/protein_id="AA69518..1"	
/db_xref="GI 710326"	
/translation="MSDDCKPFLCTAGCCQRFFINEDHLAVKHKHEMLKFGPARND	
VIVADOTENPTPLKNCNEVGFLNELASPFKKASEDDIKMPIDLSPLATPIR	
KIBPSVETTIDQSPLEPESTSDEKEPLAQTAOPTSAVRPASLQVNPLTS	
SDSVEVIIQAVPAPPTTSITOPVTPGSSPVGQPPVTPGSSPVOVOSAKMRKAALCOHPPNTGDT	
VICHGSGLVRTOESRPSLQDQPATSTETTASPAHTPTQONTSGRRRAANEDPD	
EKRKFLLRNRAASRCRKTKWQSLKDKDLSSINGQLOSEVTLRNEVAQLQ	
LJIAHKDOPVTAMOKSGEYHTAOKDSDSEEDLSPPSSPTEAICHSYSVTNSGVSSTSK	
AEAVATSVLTMADQSTEPLSQIVMAPSQRSQSGS"	
ORIGIN	
Alignment Scores:	
Pred. No.: 0.037	Length: 1520
Score: 61.00	Matches: 11
Percent Similarity: 85.71%	Conservative: 1
Best Local Similarity: 78.57%	Mismatches: 2
Query Match: 75.31%	Indels: 0
DB: 5	Gaps: 0
AAH26175_COPY_50_65 (1-16) x XIUI16158 (1-1520)	
Qy	1 GluMetThrLeuLysPheGlyProAlaArgSerLysIle 14
Db	118 GAGATGACACTGAATTGGTCAGCAGTAATGACAGTGTCTC 135
RESULT 7	
S76657	S76657 1596 bp mRNA linear ROD 07-MAY-1993
LOCUS	cyclic AMP response element DNA-binding protein isoform 1
DEFINITION	(alternative splicing product) [mice, EL4, mRNA, 1596 nt].
ACCESSION	S76657
VERSION	S76657..1 G1:243428
KEYWORDS	
SOURCE	Mus sp.
ORGANISM	Mus sp.
KEYWORDS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
REFERENCE	1 (bases 1 to 1526)
AUTHORS	Georgopoulos K., Morgan, B.A. and Moore, D.D.
TITLE	Functionally distinct isoforms of the CRE-BP DNA-binding protein mediate activity of a T-cell-specific enhancer
JOURNAL	Mol. Cell. Biol. 12 (2), 747-757 (1992)
REMARK	1511087 GenBank staff at the National Library of Medicine created this entry [NCBI Gibbs 76657] from the original journal article.
FEATURES	Location/Qualifiers
source	1..1596
/organism="Mus sp."	
/mol_type="mRNA"	
/db_xref="taxon:10095"	
gene	
CDS	
/product="cyclic AMP response element DNA-binding protein isoform 1"	
/protein_id="AA821128..1"	
/db_xref="GI 243429"	
/translation="MSDDCKPFLCTAGCCQRFFINEDHLAVKHKHEMLKFGPARND	
VIVADOTENPTPLKNCNEVGFLNELASPFKKASEDDIKMPIDLSPLATPIR	
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SDSVEVIIQAVPAPPTTSITOPVTPGSSPVGQPPVTPGSSPVOVOSAKMRKAALCOHPPNTGDT	
VICHGSGLVRTOESRPSLQDQPATSTETTASPAHTPTQONTSGRRRAANEDPD	
EKRKFLLRNRAASRCRKTKWQSLKDKDLSSINGQLOSEVTLRNEVAQLQ	
LJIAHKDOPVTAMOKSGEYHTAOKDSDSEEDLSPPSSPTEAICHSYSVTNSGVSSTSK	
AEAVATSVLTMADQSTEPLSQIVMAPSQRSQSGS"	
ORIGIN	
Alignment Scores:	
Pred. No.: 0.039	Length: 1596

Score: 61.00
 Percent Similarity: 85.71%
 Best Local Similarity: 78.57%
 Query Match: 75.31%
 DB: 9

AHH26175_COPY_50_65 (1-16) x S76657 (1-1596)

Qy 1 GluMetThrLeuLysPheGlyProAlaArgAsnSerLysIle 14
 Db 185 GAGATGACACTGAAATTGGTCAGCAGTAAATGACAGTGT 226

RESULT 8
 AX821940 LOCUS AX821940 1647 bp DNA linear PAT 10-DEC-2003
 DEFINITION Sequence 68 from Patent WO030689961.
 ACCESSION AX821940
 VERSION GI:39725161
 KEYWORDS SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Hominidae; Mammalia; Eutheria; Euarchontoglires; Primates; Cattarrhini;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Hominoidea; Homo.

REFERENCE AUTHORS Andrews, P.A., Walsh, J.A. and Gohkale, P.A.
 TITLE Method to modify differentiation of pluripotential stem cells
 JOURNAL Axordia Limited (GB)
 FEATURES SOURCE
 Qualifiers 1..1647
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN Alignment Scores:
 Pred. No.: 0.0403 Length: 1647
 Score: 61.00 Matches: 11
 Percent Similarity: 85.71% Conservative: 1
 Best Local Similarity: 78.57% Mismatches: 2
 Query Match: 75.31% Indels: 0
 DB: 6 Gaps: 0

AHH26175_COPY_50_65 (1-16) x AX821940 (1-1647)

Qy 1 GluMetThrLeuLysPheGlyProAlaArgAsnSerLysIle 14
 Db 174 GAGATGACACTGAAATTGGTCAGCAGTAAATGACAGTGT 215

RESULT 10
 AX822000 LOCUS AX822000 1647 bp mRNA linear PAT 10-SEP-1993
 DEFINITION Human mRNA for cAMP response element (CRE-BP1) binding protein.
 ACCESSION X15875
 VERSION X15875..1 GI:30214
 KEYWORDS SOURCE CREBPI gene; DNA binding protein; leucine zipper; transcription factor.
 ORGANISM Homo sapiens (human)
 Mammalia; Eutheria; Euarchontoglires; Primates; Cattarrhini;
 Hominidae; Homo.

REFERENCE AUTHORS Maekawa, T., Sakura, H., Kanai-Ishii, C., Sudo, T., Yoshimura, T., Fujisawa, J., Yoshida, M. and Ishii, S.

TITLE Leucine zipper structure of the protein CRE-BP1 binding to the cyclic AMP response element in the brain
 JOURNAL EMBO J. 8 (7), 2023-2028 (1989)
 PUBMED 2529117
 COMMENT Data kindly reviewed (20-FEB-1990) by Ishii, S.
 FEATURES Location/Qualifiers
 Source 1..1647
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="brain"
 /clone_id="Lambda gt11"
 /dev_stage="Fetus"
 /db_xref="GT:30215"
 /db_xref="GO:15136"
 /db_xref="UniProt/Swiss-Prot: P15336"
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 SALVRASLQPNVPLSISDNSSVVIQOAVPSSTSSTVITQASSNRPVPPVPEPPLI
 LHIFSGQMPVPLAPASITISNHVPAAPVLPREVMTVSFGTPGPSSPQVSEAKM
 RQGSTSRRRANEDDEKREKFLERNAASRCROKRKVYVOSLEKKAEDLISSLNG
 QLQSEVTLRNEAQQLKOLLALLAHKDPCPTAMOKSGHTADODSSEDISVPSAHPTE
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ORIGIN Alignment Scores:
 Pred. No.: 0.0403 Length: 1647
 Score: 61.00 Matches: 11
 Percent Similarity: 85.71% Conservative: 1
 Best Local Similarity: 78.57% Mismatches: 2
 Query Match: 75.31% Indels: 0
 DB: 8 Gaps: 0

AHH26175_COPY_50_65 (1-16) x HSCRBP1 (1-1647)

REFERENCE AUTHORS Andrews, P.A., Walsh, J.A. and Gohkale, P.A.
 TITLE Method to modify differentiation of pluripotential stem cells
 JOURNAL Axordia Limited (GB)
 FEATURES SOURCE
 Qualifiers 1..1647
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN

Qy	1 GluMetThrLeuIysPheGlyProAlaArgAsnSerIysIle 14	ORGANISM	Gallus gallus
Db	174 GAGATGACCTGAATTTCGTCCAGCCTTAAGCACTGTC 215		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Galliformes; Phasianidae; Phasianinae; Gallus.
RESULT 11		REFERENCE	1
DQ003047	DQ003047	AUTHORS	Huguer, S., Baguet, J., Perez, S., van Dam, H., and Castellazzi, M.
LOCUS	1768 bp mRNA	TITLE	Transcription factor ATF2 cooperates with v-Jun to promote growth factor-independent proliferation in vitro and tumor formation in vivo
DEFINITION	ATF2_var11 (ATF2) mRNA, complete cds, alternatively spliced.	JOURNAL	Mol. Cell. Biol. 18 (12), 7020-7029 (1998)
ACCESSION	DQ003047	PUBMED	9819389
KEYWORDS		REFERENCES	2 (bases 1 to 1812)
SOURCE	Homo sapiens (human)	AUTHORS	Castellazzi, M.
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.	TITLE	Direct Submission
		JOURNAL	Submitted (06-JUL-1998) M. Castellazzi, Institut National de la Sante et de la Recherche Medicale, Unite INSERM, 412 de Virologie Hunaine, Ecole Normale Superieure, 46 allee d'Italie, FRANCE
REFERENCE	1 (bases 1 to 1768)	FEATURES	Location/Qualifiers
AUTHORS	von Hippel, A.C.	source	1. . 1812
TITLE	Homo sapiens Activating Transcription Factor 2 (ATF2) mRNA Splice Variant	organism="Gallus gallus"	/mol type="mRNA"
JOURNAL	Unpublished	/product="activating transcription factor 2"	/db_xref="taxon:9031"
FEATURES	2 (bases 1 to 1768)	/protein_id="CAA78838.1"	/cell_type="fibroblast"
REFERENCE	von Hippel, A.C.	/db_xref="GOA:936012"	/dev_stage="embryo"
AUTHORS		/db_xref="InterPro:IPR004827"	1. . 1812
TITLE	Direct Submission	/db_xref="InterPro:IPR008917"	
JOURNAL	Submitted (02-APR-2005) Institute of Human Genetics, University of Heidelberg, Im Neuenheimer Feld 366, Heidelberg 69120, Germany	/db_xref="UniProt:Swiss-Prot:O93602"	
FEATURES	Location/Qualifiers	/translation="MSDDDPFLCTAPGCCQRFNTNEDHLAVKXKHMETLKFGPARNDS VIVADORTPPTRFLKNCVEGLNEALSFENETKASSEDDIKMPDLSPLATPIIR NKLBEPSVETTHODSPFLPHPESTNTDEKEVSLOQATAOPTSTIVRASPQHKGHEMTLKFGPARNDS SDSSVI IQQLIPSSTSTVITQAPSNSRIVPVGPFPFLENGQTMQVPAIASIT NSNVHVPAPVPLRVPTMPSICPGPSPQPVQEAKLRKAALQTHQPVQNTGDT AKHPGSGLMRTOSEBPPGSLQOPATSTETPASPQPOOTPTNGGRRRRAANEDPD EKREKFLLENRAAARSRCRORKVVWQKSDLLSSQVQNLQNEVNLNEAQJKO LLLAHKDCPVTAOKSGTHTADQDSSKQVQVQVPSQAKPSGS"	
REFERENCE	1 (bases 1 to 1768)	ORIGIN	AAH26175_COPY_50_65 (1-16) x GGA17724 (1-1812)
AUTHORS		Alignment Scores:	
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JOURNAL		Score:	Length: 1812
FEATURES		Percent Similarity:	61.00
REFERENCE		Best Local Similarity:	Conservative: 1
AUTHORS		Query Match:	DB: 5.31%
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TITLE		DB:	5
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AUTHORS		DB:	5
TITLE		DB:	5
JOURNAL		DB:	5
FEATURES		DB:	5
REFERENCE			

CDS

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317. .1780
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/note="contains 14 exons total; contains a nuclear
localization sequence; alternatively spliced"
/codon_start=1
/product="activating transcription factor 2 splice variant
ATF2 -var1"
/protein_id="AAV17203.1"
/db_xref="GI : 62866357"
/translation="MSDDKPKPLCTAAGCGGQRPNTEDHLAVHKHKGHEMTIKFGPARDNS
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SKIREPSVVEHTHOISPLPHPESTTSDEKEVPLAQTAAKQKPLAQTAAKQKPLAQTAAKQKPLAQTAAKQ
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SNVHYPAVPLVRPVTMVPSPVGPQGPPSPQSEAKMRKALQTHPPRNPNGDPT
VKHGEGSLVTOSEERPSQIQQPATASTTTPASPAHTTPTOTGSTSGRRRAANEDPT
EKRRKFLERNRKAASCRCRQRKQKUNVOSLLEKKAEDLSINGOLQEQVTLRNVEAQVOKQ
LILAHKDCPVTAMQRKGSQYTAODMSOTDMSOVSOPSGS"
AEAVATVTTOMADOSTERALSOITDMASPOSSOSPGS"

```

1320 Saxon

Alignment Scores:	0.0466	Length:	1883
Reduced No.:	61.00	Matches:	11
Score:	63.71*	Conservative:	1
Percent Similarity:	78.57%	Mismatches:	2
Best Local Similarity:	75.31%	Indels:	0
Query Match:	9	cons.	0

Search completed: January 12, 2006, 20:02:05
Job time : 3049 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2006, 12:45:54 (without alignments) 266.588 Million cell updates/sec

Title: AAH26175_COPY_50_65

Perfect score: 81

Sequence: 1 emt1kfpgarnskie 16

Scoring table: BLOSUM62

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Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 499697 seqs, 333236308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing First 45 summaries

Command line parameters:
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-Q=/con2/USPETO.spoof /RAWLINGS10076905/runat 10012006_144822_5310/app query.fasta_1.199
-DB=N Geneseq -QFORMAT=eastap -SUFFIX=_22n.rng -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 END=1 -MATRIX=bIoucm62 -TRANS=human40_cdi -LIST=45
-DOCIGN=00 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=L5 -MODB=LOCAL
-OUTEXT=pfo -NORM=EXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-WARN TIMEOUT=120 -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DBLEXT=7

Database : N_Geneseq_21:*

- 1: Geneseq1980s;*
- 2: Geneseq1980s;*
- 3: Geneseqm2000s;*
- 4: Geneseqn2001s;*
- 5: Geneseqm2001bs;*
- 6: Geneseqn2002as;*
- 7: Geneseqn2002bs;*
- 8: Geneseqm2003as;*
- 9: Geneseqm2003bs;*
- 10: Geneseqn2003cb;*
- 11: Geneseqm2003ds;*
- 12: Geneseqn2004as;*
- 13: Geneseqn2004bs;*
- 14: Geneseqm2005s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		
Result No.	Score	Query Match Length DB ID Description
1	61	75.3 1518 14 ADV42650 Human psy
2	61	75.3 1647 10 ADK67038 Gene #128
3	61	75.3 1647 10 ADK66978 Gene #68
4	61	75.3 1852 10 ADB53173 Primary r

ALIGNMENTS

RESULT 1

ADV42650	standard; cdna; 1518 BP.
ID	ADV42650
XX	
AC	ADV42650;
XX	
DT	10-MAR-2005 (first entry)
XX	
DB	Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 278.
XX	
KW	microarray; psychoneuroendocrinimmune; chronic fatigue; non-insulin dependent diabetes; allergy; immune disorder; inflammation; cancer; neoplasm; infection; expressed sequence tag; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO2004108899-A2.
XX	
PD	16-DEC-2004.
XX	
PF	04-JUN-2004; 2004WO-US017686.
XX	
PR	04-JUN-2003; 2003US-047591P.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Nicholson A, Vernon SD;
XX	

CC markers for the prediction or identification of the physiological state
 CC of tissue or cell sample that has been exposed to a compound, or to
 CC identify or predict the toxic effects of a compound or an agent. These
 CC may also be used as markers for monitoring toxicity progression or for
 CC drug screening. The present sequence represents a primary rat hepatocyte
 CC toxicity modelling related gene sequence from the present invention.
 XX SQ Sequence 1852 BP; 558 A; 472 C; 405 G; 417 T; 0 U; 0 Other;

RESULT 4
 ADB53173 standard; DNA; 1852 BP.
 ADB53173;
 DB 04-DEC-2003 (First entry)

Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3715.
 toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
 toxicity marker; toxicity progression; drug screening;
 primary rat hepatocyte toxicity modelling; gene; ds.

Rattus norvegicus.
 WO2003065993-A2.
 14-AUG-2003.

04-FEB-2003; 2003WO-US0003482.

04-FEB-2002; 2002US-0353171P.
 13-MAR-2002; 2002US-0363534P.
 08-APR-2002; 2002US-0370248P.
 10-APR-2002; 2002US-0371144P.
 10-APR-2002; 2002US-0371155P.
 11-APR-2002; 2002US-0371413P.
 19-APR-2002; 2002US-0373601P.
 19-APR-2002; 2002US-0373602P.
 22-APR-2002; 2002US-0373119P.
 08-MAY-2002; 2002US-0378370P.
 09-MAY-2002; 2002US-0378632P.
 09-MAY-2002; 2002US-0378653P.
 09-JUL-2002; 2002US-0378665P.
 09-JUL-2002; 2002US-0394230P.
 04-SEP-2002; 2002US-0407638P.
 28-JAN-2003; 2003US-0442900P.

(GENE-) GENE LOGIC INC.

Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
 I Elashoff M;
 I WPI: 2003-731472/69.

Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox mean values.

Claim 44; SEQ ID NO 3715; 874PP; English.

The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity genes.

RESULT 5
 AAH26175_COPY_50_65 (1-16) x ADB53173 (1-1852)
 Qy 1 GluMetThrLeuIysPheGlyProAlaArgAsnSerLysIle 14
 Db 432 GAGATGACACTGAAATTGGTCAGCTTAATGACAGTGTCA 473

RESULT 5
 ADC22243 standard; DNA; 51 BP.
 ID ADC22243;
 XX AC ADC22243;
 XX DT 18-DEC-2003 (first entry)
 XX DE Protein binding domain nucleotide sequence SEQ ID NO:92.
 XX KW recombinant fusion protein; fusion protein; binding; detection;
 XX localisation domain; binding domain;
 XX subcellular compartment localisation; gene; ds.
 XX OS Homo sapiens.
 PN WO2003012068-A2.
 XX PD 13-FEB-2003.
 XX PP 01-AUG-2002; 2002WO-US024572.
 XX PR 01-AUG-2001; 2001US-0309355P.
 PR 13-DEC-2001; 2001US-0341599P.
 PA (CELL-L) CELLOMICS INC.
 PI Bright G, Premkumar DR, Chen Y;
 XX DR WPI; 2003-248174/24.
 XX DR P-PSD; ADC22242.

New recombinant fusion protein comprising detection and first localization domains and a binding domain for the molecule of interest, useful for detecting binding of a molecule of interest.

Disclosure; SEQ ID NO 92; 101PP; English.

The present invention describes a recombinant fusion protein (I) for detecting binding of a molecule of interest. (II) comprises: (a) a detection domain; (b) a first localisation domain; and (c) a binding domain for the molecule of interest. The detection domain, the first localisation domain and the binding domain for the molecule of interest constituting the recombinant fusion protein for detecting binding of a molecule of interest are operably linked. The binding domain for the first localisation domain for the molecule of interest is separated from the first localisation domain and the binding domain for the molecule of interest both do not occur in a single non-combining domain with the same molecule of interest. Also described is a recombinant protein with the same molecule of interest. The recombinant protein for detecting binding of a molecule of interest.

(1) a recombinant nucleic acid encoding the recombinant fusion protein;
 CC (2) a recombinant expression vector comprising the nucleic acid control
 CC sequences operably linked to the recombinant nucleic acid molecule; (3) a
 CC genetically engineered host cell transfected with the recombinant
 CC expression vector; (4) a kit for detecting binding of the molecule of
 interest; and (5) a method for identifying compounds that alter the
 CC binding of the molecule of interest. The recombinant fusion protein is
 useful for detecting binding of a molecule of interest. The recombinant
 CC fusion protein eliminates the need to construct two or more chimeric
 CC proteins and enables the monitoring of biochemical events in live, intact
 CC or fixed cells. The present sequence is used in the exemplification of
 the present invention.

SQ Sequence 51 BP; 20 A; 10 C; 9 G; 12 T; 0 U; 0 Other;

Alignment Scores:	
Pred. No. :	0.00398
Score:	58.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	71.60%
DB:	10

AAH26175_COPY_50_65 (1-16) × ADC22243 (1-51)

QY	1 GluMetThrLeuLysPheGlyProAlaArgAsn 11
	19 GAGATGACATGAATTGGTCCAGACGTAAAT 51

RESULT 6

AAS61674	AAS61674 standard; cDNA; 501 BP.
----------	----------------------------------

XX	AAS61674;
XX	DT 29-JAN-2002 (first entry)
DB	Lung small cell carcinoma antigen, cDNA #215.
XX	Human; cytosstatic; antitumour; lung small cell cancer antigen; tumour; lung cancer; ss.
OS	Homo sapiens.
PN	W0200177168-A2.
XX	18-OCT-2001.
PD	06-SEP-2000.
PP	21-FEB-2000; 2000EP-00200610.
XX	PR 26-FEB-1999; 99US-0122487P.
PR	PR (GEST) GENSET.
XX	XX (PI Dumas Milne Edwards J, Ducleart A, Giordano J; XX DR WPI: 2000-500381/45.
PA	DR P-PSDB; AAC02942.

(CORYX CORP.

XX	Lung tumor polynucleotide and polypeptides useful in therapy and diagnosis of cancer especially lung cancer.
----	--

PT PI Lodes MJ, Wang T, Mohamath R, Indirias CY;

XX PS XX DR WPI: 2002-010896/01.

PT PT XX PS XX DR WPI: 2002-010896/01.

The invention relates to novel isolated lung small cell cancer antigen polynucleotides (I) and polypeptides (II) used in a method of detecting cancer in a patient. The method is optionally performed by utilising oligonucleotides (III), where the biological sample from the patient is

CC contacted with (III), detecting the amount of polynucleotide hybridised to (III) in the sample and comparing the amount of polynucleotide to a CC predetermined cut-off value and thereby determining cancer in a patient. CC (I), (II) or antigen-presenting cells expressing (II) is useful for CC stimulating and/or expanding T cells specific for a tumour protein. The CC method comprises contacting T cells with one of the components under CC conditions to permit the stimulation and/or expansion of the cells. A CC composition comprising (I) is useful for stimulating the development of a cancer especially CC in a patient and for inhibiting the development of a cancer especially CC lung cancer in a patient. An isolated T cell population is useful for CC removing tumour cells from the biological sample and for inhibiting the CC development of cancer in a patient. AAC61460-AAS61874 represent novel CC human lung small cell cancer antigen coding sequences of the invention CC XX SQ Sequence 501 BP; 151 A; 103 C; 121 G; 125 T; 0 U; 1 Other;

SQ Alignment Scores:

Pred. No. :	0.00398
Score:	58.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	71.60%
DB:	10

AAH26175_COPY_50_65 (1-16) × AAS61674 (1-501)

QY	1 GluMetThrLeuLysPheGlyProAlaArgAsnSerLysIle 14
	1 ::::: 14
Db	414 GAGATGACACTGAATTGGTCCANACGTAAATTGTCAGCTGTC 455

RESULT 7

ID AAC02948	standard; cDNA; 229 BP.
XX	XX AAC02948;
AC	AC AAC02948;

XX	XX DT 06-OCT-2000 (first entry)
DB	DB Human secreted protein 5' EST, SEQ ID NO: 2946.

XX	XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
KW	KW gene therapy; chromosome mapping; ss.
XX	XX OS Homo sapiens.
OS	OS XX EP1033401-A2.

PN	PN XX PR 06-SEP-2000.
XX	XX PR 21-FEB-2000; 2000EP-00200610.
PD	PD XX PR 26-FEB-1999; 99US-0122487P.

PP	PP XX PA (GEST) GENSET.
XX	XX PI Dumas Milne Edwards J, Ducleart A, Giordano J; XX DR WPI: 2000-500381/45.

DR WPI: 2000-500381/45.

DR P-PSDB; AAC02942.

PT PT XX PS XX DR WPI: 2002-010896/01.

The present sequence is one of a large number of 5' ESTs derived from the mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or poly+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of

CC menas and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from cDNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.

XX Sequence 229 BP; 63 A; 50 C; 67 G; 48 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 0.0989 Length: 229
Score: 55.00 Matches: 10
Percent Similarity: 78.57% Conservative: 1
Best Local Similarity: 71.43% Mismatches: 3
Query Match: 71.43% Indels: 0
DB: 67.90% Gaps: 0

AAH26175_COPY_50_65 (1-16) × AAC02948 (1-229)

QY 1 GluMetThrLeuIysPheGlyProAlaArgAsnSerLysIle 14
Db 165 GAGATGACATTGGAATTGGCCAGGAACTGACTCACTCAGTC 206

RESULT 8 ABV2893 standard; cDNA: 800 BP.

XX ID ABV2893

AC ABV2893;

XX DT 16-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 28984.

DE Human prostate expression marker cDNA 28984.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX pharmacogenomic marker; gene; ss.

XX Homo sapiens.

OS WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US005171.

XX PR 17-FEB-2000; 2000US-0183319P.

XX PR 16-MAR-2000; 2000US-018962P.

XX PR 25-MAY-2000; 2000US-020754P.

XX PR 09-JUN-2000; 2000US-021114P.

XX PR 18-JUL-2000; 2000US-021907P.

XX PR 13-DEC-2000; 2000US-0255381P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;

XX XX XX XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX XX XX DR 2001-662795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1: Page 6132; 11750PP; English.

XX PT The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) selecting a composition for inhibiting prostate cancer in a patient; (e) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodynamic or pharmacogenomic marker

XX CC

SQ Sequence 800 BP; 244 A; 147 C; 224 T; 0 U; 11 Other;
 Alignment Scores:
 Pred. No.: 0.455 Length: 800
 Score: 55.00 Matches: 10
 Percent Similarity: 78.57% Conservative: 1
 Best Local Similarity: 71.43% Mismatches: 3
 Query Match: 67.90% Indels: 0
 DB: 5 Gaps: 0

AAH26175_COPY_50_65 (1-16) × ABV23152 (1-800)

Qy 1 GluMetThrLeuLysPheGlyProAlaArgABNSerLysIle 14
 Db 179 GAGATGACATGGAAATTGGCCAGGCCAGCTGACTCACTGC 220

RESULT 10
 ADP80924
 ID ADP80924 standard; cDNA; 1239 BP.
 XX AC ABV28463
 XX DT ABV28463 standard; cDNA; 2755 BP.
 XX DT ABV28463;
 XX DT 16-SEP-2002 (First entry)
 DE Human prostate expression marker cDNA 28454.
 XX DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW KW pharmacogenomic marker; gene; 88.
 OS OS Homo sapiens.
 XX PN WO200160860-A2.
 XX PN 23-AUG-2001.
 XX FD 20-FEB-2001; 2001WO-US005171.
 XX PF 17-FEB-2000; 2000US-0183319P.
 XX PR 16-MAR-2000; 2000US-0189662P.
 XX PR 25-MAY-2000; 2000US-020754P.
 XX PR 09-JUN-2000; 2000US-0211314P.
 XX PR 18-JUL-2000; 2000US-0219007P.
 XX PR 13-DEC-2000; 2000US-0255281P.
 XX PA (MILLI-) MILLENIUM PREDICTIVE MEDICINE INC.
 XX PI Schliegel R, Endege WO, Monahan JE;
 XX DR WPI; 2001-662795/76.
 XX PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX
 XX Claim 1; Page 5940-5941; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV2213) of the
 CC specification or its complement. (1) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX SQ Sequence 2755 BP; 645 A; 811 C; 612 G; 684 T; 0 U; 3 Other;
 CC interact with c-fos in the exemplification of the present invention.

Pred. No.: 2.06 Length: 2755 Query Match: 67.90% Indels: 0
Score: 55.10 Matches: 10 Gaps: 0
Percent Similarity: 78.57% Conservative: 1 DB: ABV22640 (1-2755)
Best Local Similarity: 71.43% Mismatches: 3
DB: ABV22640 (1-2755) Indels: 0
Query Match: 67.90% Gaps: 0
DB: ABV22640 (1-2755) Mismatches: 3
Indels: 0
Gaps: 0

Qy 1 GluMetThrLeuLysPheGlyProAlaArgAsnSerLysIle 14 Qy 1 GluMetThrLeuLysPheGlyProAlaArgAsnSerLysIle 14
Db 194 GAGATGACTTGAATTGGCCCAACTGACTCGTC 235 Db 194 GAGATGACATTTGCCCCAACTGACTCGTCAGTCAGTC 235

RESULT 12
ABV22640 Standard, cDNA, 2755 BP.
ID ABV22640 DE Human SIRS/sepsis diagnostic marker DNA fragment 6337.
XX AC XX Systemic inflammatory response syndrome; SIRS; antibacterial;
XX DT 13-SEP-2002 (first entry) KW immunosuppressive; antiinflammatory; diagnose; sepsis; ds.
XX XX
DE Human prostate expression marker cDNA 22631.
XX KW Human: prostate cancer; cytosstatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PD 14-OCT-2004.
XX DT 02-JUN-2005 (first entry)
XX DE Human SIRS/sepsis diagnostic marker DNA fragment 6337.
XX AC XX Systemic inflammatory response syndrome; SIRS; antibacterial;
XX KW immunosuppressive; antiinflammatory; diagnose; sepsis; ds.
XX OS Homo sapiens.
XX PN WO2004087949-A2.
XX PR 02-APR-2003; 2003DB-01015031.
XX PR 08-AUG-2003; 2003DE-0103511.
XX PR 02-SEP-2003; 2003DE-0104395.

RESULT 13
ABV22640 Standard, cDNA, 2755 BP.
ID ABV22640 DE Human SIRS/sepsis diagnostic marker DNA fragment 6337.
XX AC XX Systemic inflammatory response syndrome; SIRS; antibacterial;
XX KW immunosuppressive; antiinflammatory; diagnose; sepsis; ds.
XX OS Homo sapiens.
XX PD 14-OCT-2004.
XX DT 31-MAR-2004; 2004WO-BP002419.
XX DE Human SIRS/sepsis diagnostic marker DNA fragment 6337.
XX AC XX Systemic inflammatory response syndrome; SIRS; antibacterial;
XX KW immunosuppressive; antiinflammatory; diagnose; sepsis; ds.
XX OS Homo sapiens.
XX PN WO20040860-A2.
XX PR 02-APR-2003; 2003DB-01015031.
XX PR 08-AUG-2003; 2003DE-0103511.
XX PR 02-SEP-2003; 2003DE-0104395.

(SIRS-) SIRS LAB GMBH.
PA XX
PI Russwurm S, Reinhart K, Saluz H, Straube B, Zipfel PF, Deigner H;
XX DR WPI; 2004-748070/73.
XX PT In vitro detection of systemic inflammatory response syndrome and related
PT conditions, for e.g. monitoring progression, comprises detecting abnormal
PT expression of disease-related genes.
XX Disclosure; Page: 75pp; German.
XX PS
XX CC The invention relates to a novel method for in vitro detection of
CC systemic inflammatory response syndrome (SIRS). The method comprises
CC detecting abnormal expression of disease-related genes or their
CC associated peptides. The method of the invention demonstrates
CC antibacterial, immunosuppressive and antiinflammatory applications and
CC may be used for early differential diagnosis, monitoring progression,
CC assessing risk, assessing the likely response to treatment and for post
CC preparation of agents for treatment or prevention of the specified
CC disease. The current sequence is that of a human SIRS/sepsis diagnostic
CC peptide-like conditions. The recombinant or synthetic nucleic acid
CC sequences of the invention, or derived proteins or peptides, may be
CC useful as calibrants in assays for the specified diseases, for evaluating
CC activity or toxicity in screening for active agents and/or for
CC preparing agents for treatment or prevention of the specified
CC disease. The current sequence is that of a human SIRS/sepsis diagnostic
CC marker DNA fragment of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at <http://wipo.int/pub/published-pct-sequences>. Furthermore, a number of arbitrary SEQ ID NO's are
CC disclosed within the specification, however, these have not been taken
CC into account during indexing due to inconsistencies in application and
CC format
XX SQ Sequence 2758 BP; 647 A; 813 C; 612 G; 686 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.06 Length: 2755
Score: 55.00 Matches: 10
Percent Similarity: 78.57% Conservative: 1
Best Local Similarity: 71.43% Mismatches: 3

Percent Similarity: 78.57%
 Best Local Similarity: 71.43%
 Query Match: 67.90%
 DB: 13 AAH26175_COPY_50_65 (1-16) x ACP87477 (1-2758)
 Qy 1 GluMetThrLeuLysPheGlyProAlaArgAsnSerLysIle 14
 Db 197 GAGATGACATTGAAATTGGCCAGGCCGAACTGACTCAAGTC 238

RESULT 14
 ADC22231 ID ADC22231 standard; DNA; 51 BP.
 XX AC ADC22231;
 XX DT 18-DEC-2003 (first entry)
 DE Protein binding domain nucleotide sequence SEQ ID NO:80.
 XX KW recombinant fusion protein; fusion protein; binding; detection;
 KW localisation domain; binding domain;
 KW subcellular compartment localisation; gene; ds.
 XX OS Homo sapiens.
 XX PN WO2003012068-A2.
 XX PD 13-FEB-2003.
 XX PP 01-AUG-2002; 2002WO-US024572.
 XX PR 01-AUG-2001; 2001US-0309395P.
 XX PR 13-DEC-2001; 2001US-0341585P.
 XX PA (CELL-) CELLOMICS INC.
 XX Bright G, Premkumar DR, Chen Y;
 XX WPI: 2003-248174/24.
 DR P-PSDB; ADC2230.
 XX New recombinant fusion protein comprising detection and first
 PT localization domains and a binding domain for the molecule of interest,
 PT useful for detecting binding of a molecule of interest.
 Disclosure: SEQ ID NO 80; 101pp; English.
 XX PS
 XX DR
 CC The present invention describes a recombinant fusion protein (I) for
 CC detecting binding of a molecule of interest, (I) comprises: (a) a
 CC detection domain; (b) a first localisation domain; and (c) a binding
 CC domain for the molecule of interest. The detection domain, the first
 CC localisation domain and the binding domain for the molecule of interest
 CC constituting the recombinant fusion protein for detecting binding of a
 CC molecule of interest are operably linked. The binding domain for the
 CC molecule of interest is separated from the first localisation domain by 0
 CC -20 amino acid residues. The first localisation domain and the binding
 CC domain for the molecule of interest both do not occur in a single non-
 CC recombinant protein with the same spacing as in the recombinant fusion
 CC protein for detecting binding of a molecule of interest. Also described:
 CC (1) a recombinant nucleic acid encoding the recombinant fusion protein;
 CC (2) a recombinant expression vector comprising the nucleic acid control
 CC sequences operably linked to the recombinant nucleic acid molecule; (3) a
 CC genetically engineered host cell transfected with the recombinant
 CC expression vector; (4) a kit for detecting binding of the molecule of
 CC interest; and (5) a method for identifying compounds that alter the
 CC binding of the molecule of interest. The recombinant fusion protein is
 CC useful for detecting binding of a molecule of interest. The recombinant
 CC fusion protein eliminates the need to construct two or more chimeric
 CC proteins and enables the monitoring of biochemical events in live, intact
 CC or fixed cells. The present sequence is used in the exemplification of
 CC the present invention.

XX SQ Sequence 51 BP; 18 A; 12 C; 10 G; 11 T; 0 U; 0 Other;
 Conservative: 1
 Mismatches: 3
 Indels: 0
 Gaps: 0

Alignment Scores:
 Pred. No.: 0.063 Length: 51
 Score: 52.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 64.20% Indels: 0
 DB: 10 Gaps: 0

AAH26175_COPY_50_65 (1-16) x ADC22231 (1-51)

Qy 1 GluMetThrLeuLysPheGlyProAlaArgAsnSerLysIle 14
 Db 19 GAGATGACATTGAAATTGGCCAGGCCGAACTGACTCAAGTC 48

RESULT 15
 ABV1146 ID ABV1146 standard; cDNA; 397 BP.
 XX AC ABV1146;
 XX DT 13-SEP-2002 (first entry)
 XX DB Human prostate expression marker cDNA 14137.
 XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX OS Homo sapiens.
 XX PN WO200160860-A2.
 XX PD 23-AUG-2001.
 XX PF 20-FEB-2001; 2001WO-US005171.
 XX PR 17-FEB-2000; 2000US-0183319P.
 PR 16-MAR-2000; 2000US-018962P.
 PR 25-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-0255581P.
 XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX PI Schlegel R, Endege WO, Monahan JE;
 XX DR WPI; 2001-662795/76.
 XX PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX PS Claim 1; Page 2358; 11750pp; English.
 XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX SQ Sequence 397 BP; 118 A; 87 C; 96 G; 96 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	12.2	Length:	397
Score:	46.00	Matches:	9
Percent Similarity:	90.00%	Conservative:	0
Best Local Similarity:	90.00%	Mismatches:	1
Query Match:	56.79%	Indels:	0
DB:	5	Gaps:	0
AHH26175_COPY_50_65 (1-16) x ABY14146 (1-397)			
Qy	1 GluMetThrLeuLysPheClyProAlaArg 10		
Db	162 GAGATGACTTGAAATTGGCCCATACCGA 191		

Search completed: January 12, 2006, 19:11:14
Job time : 406 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2006, 17:58:06 ; Search time 2605 Seconds

(without alignments)
287.258 Million cell updates/sec

Title: AAH26175_COPY_50_65

Perfect score: 81

Sequence: 1 emtikfgparnskie 16

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4107832 seqs, 2339541228 residues

Total number of hits satisfying chosen parameters:

82156650

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing First 45 summaries

Command line parameters:

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-MODEL:frame+P2N.model -DEV=x1h
-Q=/cmr2_1/spool/RAWLINGS/0076905/runat_10012006_144824_5333/app/query.fasta_1.199
-DB=EST -QMTM=fastap -SUFFIXX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=000 -THR SCORE=pcit -THR MAX=100 -THR MIN=0 -MODE=LOCAL
-OUTENT=pfo -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER:RAWLINGS/0076905@CGN_1..15315 @runat_10012006_144824_5333 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : EST:*

1: 9b_est1:*

2: 9b_est2:*

3: 9b_est3:*

4: 9b_htc:*

5: 9b_est4:*

6: 9b_est5:*

7: 9b_est6:*

8: 9b_est7:*

9: 9b_g982:*

10: 9b_g982:*

11: 9b_g983:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match Length	DB ID	Description
1	61 75.3	340	AA14544	AA414544 vc60a12_B
2	61 75.3	344	AM0769431	CL569431 AM0769431 Sa
3	61 75.3	417	CC249614	CC249614 XI426 Bay
4	61 75.3	506	AJ448042	AJ448042 AJ448042
5	61 75.3	508	CR542857	CR542857 DKPZP451L
6	61 75.3	515	CD693411	CD693411 EST9934 h
7	61 75.3	538	AU279581	AU279581

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

** Summarized by the program.

*** Summarized by the program.

**** Summarized by the program.

***** Summarized by the program.

Scoring table: BLOSUM62	8	61	75.3	571	1	AJ450203
Ygapop 10.0 , Xgapext 0.5	9	61	75.3	576	3	BP257160
Ygapop 10.0 , Ygapext 0.5	10	61	75.3	577	3	CN367889
Fgapop 6.0 , Fgapext 7.0	11	61	75.3	582	3	BP201994
Delop 6.0 , Delext 7.0	12	61	75.3	606	3	BQ037883
Scoring table: BLOSUM62	13	61	75.3	613	5	BQ662818
Scoring table: BLOSUM62	14	61	75.3	621	7	CN367892
Scoring table: BLOSUM62	15	61	75.3	635	1	AU119505
Scoring table: BLOSUM62	16	61	75.3	637	5	BY736938
Scoring table: BLOSUM62	17	61	75.3	640	7	CN455108
Scoring table: BLOSUM62	18	61	75.3	642	7	BB628862
Scoring table: BLOSUM62	19	61	75.3	650	2	CN367893
Scoring table: BLOSUM62	20	61	75.3	651	6	CB438334
Scoring table: BLOSUM62	21	61	75.3	653	2	BB627898
Scoring table: BLOSUM62	22	61	75.3	653	6	CD355777
Scoring table: BLOSUM62	23	61	75.3	662	6	CD355777
Scoring table: BLOSUM62	24	61	75.3	664	6	CP535749
Scoring table: BLOSUM62	25	61	75.3	669	2	BB665053
Scoring table: BLOSUM62	26	61	75.3	669	5	BY734700
Scoring table: BLOSUM62	27	61	75.3	669	20	BY739920
Scoring table: BLOSUM62	28	61	75.3	670	7	CN367891
Scoring table: BLOSUM62	29	61	75.3	686	2	BB882633
Scoring table: BLOSUM62	30	61	75.3	716	12	BF613172
Scoring table: BLOSUM62	31	61	75.3	722	6	CP532094
Scoring table: BLOSUM62	32	61	75.3	723	7	CN454827
Scoring table: BLOSUM62	33	61	75.3	737	8	CK634639
Scoring table: BLOSUM62	34	61	75.3	742	7	CK634639
Scoring table: BLOSUM62	35	61	75.3	744	1	AJ453735
Scoring table: BLOSUM62	36	61	75.3	746	6	CD348287
Scoring table: BLOSUM62	37	61	75.3	749	6	CD348288
Scoring table: BLOSUM62	38	61	75.3	758	6	CA510974
Scoring table: BLOSUM62	39	61	75.3	758	6	CB521135
Scoring table: BLOSUM62	40	61	75.3	781	6	CA512317
Scoring table: BLOSUM62	41	61	75.3	782	6	CD348295
Scoring table: BLOSUM62	42	61	75.3	792	7	CR629546
Scoring table: BLOSUM62	43	61	75.3	802	7	CR629544
Scoring table: BLOSUM62	44	61	75.3	805	1	AJ454932
Scoring table: BLOSUM62	45	61	75.3	806	6	CB961368

ALIGNMENTS

RESULT 1	AA414544	340 bp	mRNA	linear	EST 04-AUG-1997
LOCUS	AA414544				
DEFINITION	vc0a12_s1	Knowles Soliter mouse 2 cell Mus musculus cDNA clone			
		IMAGE:78942_5			
		Similar to 9b: M77167 Mouse T-cell antigen receptor alpha-chain (MOUSE)_ mRNA sequence.			
ACCESSION	AA414544				
VERSION	AA14544.1	GI:2014680			
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomii; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Muridae; Murinae; Mus.				
REFERENCE	Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Scheibenbogen, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theisinger, B., Wylie, T., Lennon, G., Soates, B., Wilson, R. and Waterston, R.				
TITLE	The WashU-HMM Mouse EST Project				
JOURNAL	Unpublished (1996)				
COMMENT	Contact: Marra M./Mouse EST Project				
	WashU-HMM Mouse EST Project				
	Washington University School of Medicine				
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				
	Tel: 314 286 1800				
	Fax: 314 286 1810				
	Email: mouseest@watson.wustl.edu				
	This clone is available royalty-free through LMMU; contact the IMAGE Consortium (info@image.llnl.gov) for further information.				

DEFINITION	AJ448042 riken Gallus gallus cDNA clone 18i13r1, mRNA sequence.	FEATURES	Source	information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/ .
VERSION	AJ448042.1 GI:20215263			Location/Qualifiers
KEYWORDS				1..508
ORGANISM	Gallus gallus (chicken)			/organism="Pongo pygmaeus"
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			/mol_type="mRNA"
	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;			/db_xref="taxon:3600"
	Phasianinae; Gallus.			/clone="DKFZp159L240"
	1 (bases 1 to 506)			/tissue_type="cortex"
REFERENCE	Buerstedde, J.M.			/dev_stage="adult"
AUTHORS				/lab_host="DIL0B"
TITLE	Gallus gallus bursal lymphocyte EST			/clone_lib="#459 (synonym: pcorl)"
JOURNAL	Unpublished (2002)			/note="Vector: pSport1_Sfi; site_1: SfiIA; site_2: SfiIB"
COMMENT	Contact: Buerstedde JM			
	Cellular Immunology Heinrich-Pette-Institute			
	Martinisir, 52, 20251 Hamburg, Germany			
	Email: http://genetics.hpi.uni-hamburg.de/dt40est.html .			
FEATURES	Location/Qualifiers			
Source	1..506			
	/organism="Gallus gallus"			
	/mol_type="mRNA"			
	/db_xref="taxon:9031"			
	/clone="8131"			
	/cell_types="bursal lymphocyte"			
	/dev_stage="2-3 weeks old"			
	/clone_lib="rikene1"			
	/note="CB inbred strain"			
ORIGIN				
	Alignment Scores:			RESULT 6
Pred. No.:	0.313	Length:	CD633411	CD693411
Score:	61.00	Matches:	EST9934	515 bp mRNA linear EST 25-JUN-2003
Percent Similarity:	85.71%	Conservative:	EST	mRNA sequence.
Best Local Similarity:	78.57%		CD693411.1	
Query Match:	75.31%		GI:32217044	
DB:	1		EST.	
KEYWORDS			Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.	
ORGANISM	Homo sapiens (human)			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
	Hominidae; Homo			
REFERENCE	1 (bases 1 to 515)			
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
	Transcriptional Gene Expression Profile of Human Nasopharynx Unpublished (2003)			
	Contact: Yixin Zeng			
	Cancer Center			
	Sun Yat-sen University			
	651 DongRong Road East, Guangzhou 510060, China			
	Tel: 86-1380-9770-743			
	Fax: 86-20-8775-4506			
FEATURES	Source			
	Yxxzeng@gzams.edu.cn.			
	Location/Qualifiers			
	1..515			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:606"			
	/tissue_type="normal nasopharynx"			
	/clone_lib="human nasopharynx"			
	/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"			
ORIGIN				
	Alignment Scores:			
Pred. No.:	0.319	Length:	CD693411	CD693411
Score:	61.00	Matches:	EST9934	508 bp mRNA linear EST 07-JUL-2004
Percent Similarity:	85.71%	Conservative:	EST	mRNA sequence.
Best Local Similarity:	78.57%		CD693411.1	
Query Match:	75.31%		GI:49894012	
DB:	1		EST.	
KEYWORDS				
ORGANISM	Pongo pygmaeus (orangutan)			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
	Hominoidea; Pongo.			
REFERENCE	1 (bases 1 to 506)			
AUTHORS	Boecker,H., Boecker,M., Brandt,P., Weil,B., Amid,C., Ossanger,A., Fobo,G., Ian,M. and Wiemann,S.			
TITLE	Pongo pygmaeus mRNA (Bioeker,H., Boecker,M., Brandt,P., et al.)			
JOURNAL	Unpublished (2004)			
COMMENT	Contact: MIPS			
	Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany			
	This is the 5' sequence of the clone insert Clone from S. Wiemann,			
	Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: S.wiemann@dkfz-heidelberg.de; Generated by GSF (National			
	Research Centre for Biotechnology Ltd., Braunschweig/Germany)			
	Within the CDNA sequencing consortium of the German Genome Project.			
	This clone (DKFZp159L240) is available at the RZPD in Berlin.			
	Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clione@rzpd.de Further			

Pred. No.:	0_363	Length:	576	ACCESSION	BP201994
Score:	61.00	Matches:	11	VERSION	BP201994.1
Percent Similarity:	85.71%	Conservative:	1	KEYWORDS	GI:52052519
Best Local Similarity:	85.71%	Mismatches:	2	SOURCE	Homo sapiens (human)
Query Match:	78.57%	Indels:	0	ORGANISM	Homo sapiens
DB:	75.31%	Gaps:	0	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
AAH26175_COPY_50_65 (1-16) × BP257160 (1-576)				REFERENCE	1 (bases 1 to 582)
Qy	1 GluMetThrLeuIysPheGlyProAlaArgAsnSerLysIle 14			AUTHORS	Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,, Nakai,K. and Sugano,S.
Db	410 GAGATGACACTGAAATTGGTCCAGCACTGAATGACAGTGTC 451			TITLE	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
RESULT 10				JOURNAL	Genome Res. 14 (9), 1711-1718 (2004)
CN3_67889	CN3_67889 577 bp mRNA Homo sapiens EST 16-MAY-2004			PUBMED	15342556
LOCUS	DEFINITION GRN_ES Homo sapiens cDNA 5', mRNA sequence.			COMMENT	Contact : Yutaka Suzuki
ACCESSION CN3_67889	VERSION CN3_67889.1	EST: GI:47367823		DEFINITION	Institute of Virology
SOURCE	ORGANISM			LOCATION	Institute of Medical Science, University of Tokyo
Homo sapiens (human)	Homo sapiens			4-6-1,	Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				Email:	Ysuzuki@imrc.u-tokyo.ac.jp.
REFERENCE	AUTHORS			FEATURES	1 . 582
Li,Y., Xu,C., Pang,R., Guegler,K., Rao,M.S., Mandelam,R., Lebski,J. and Stanton,L.W.				Source	/organism="Homo sapiens"
TITLE					/mol type="mRNA"
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation					/db_xref="taxon:9606"
JOURNAL					/clone "AMR07079"
PUTMED					/cione_id="Stugano CDNA library, amygdala"
COMMENT					
Insert Length: 577 Std Error: 0.00.				ORIGIN	
FEATURES	Source			Alignment Scores:	
1..577 /organism="Homo sapiens"				Pred. No.:	0.367
/mol type="mRNA"				Score:	61.00
/db_xref="taxon:9606"				Percent Similarity:	85.71%
/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"				Best Local Similarity:	78.57%
/clone lib="GRN_ES"				Query Match:	75.31%
/note="Oligo dT primed, full-length enriched cDNA library from undifferentiated HES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"				DB:	0
ORIGIN				RESULT 12	AAH26175_COPY_50_65 (1-16) × BP201994 (1-582)
Alignment Scores:				Qy	1 GluMetThrLeuIysPheGlyProAlaArgAsnSerLysIle 14
Pred. No.:	0_364	Length:	577	Db	433 GAGATGACACTGAAATTGGTCCAGCACTGAATGACAGTGTC 474
Score:	61.00	Matches:	11	DEFINITION	BQ037883
Percent Similarity:	85.71%	Conservative:	1	LOCUS	606 bp mRNA linear EST 01-MAY-2002
Best Local Similarity:	85.71%	Mismatches:	2	DEFINITION	pgnic-pgo07-j22 normalized chicken lymphoid cDNA library Gallus gallus cDNA clone pgnic-pgo07-j22 5' similar to ref NP_001871.1 (NM_001880) activating transcription factor 2; cAMP-response element-binding protein-2; cAMP responsive element binding protein 2 [Homo sapiens] Pir (S05380 transcription factor ATF2 - human emb CAA3886.1 (X15875) CAMP response, mRNA sequence.
Query Match:	75.31%	Indels:	0	ACCESSION	BQ037883
DB:	7	Gaps:	0	VERSION	BQ037883.2
AAH26175_COPY_50_65 (1-16) × CN367889 (1-577)				KEYWORDS	GI:20182615
Qy	1 GluMetThrLeuIysPheGlyProAlaArgAsnSerLysIle 14			SOURCE	EST
Db	289 GAGATGACACTGAAATTGGTCCAGCACTGAATGACAGTGTC 330			ORGANISM	Gallicus gallus (chicken)
RESULT 11				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.	
BP201994	BP201994 582 bp mRNA linear EST 14-SEP-2004			REFERENCE	1 (bases 1 to 606)
LOCUS	BP201994 Sugano cDNA library, amygdala Homo sapiens cDNA clone AMR07079, mRNA sequence.			AUTHORS	Morgan,R.W. and Burnside,J.
DEFINITION				TITLE	Chicken Lymphoid ESTs
				JOURNAL	Unpublished (2001)
				COMMENT	On Mar 27, 2002 this sequence version replaced gi:197714231.
					Contact: Joan Burnside
					Molecular Endocrinology
					University of Delaware
					40 Townsend Hall, Newark, DE 19717, USA
					Tel: 302-831-1345
					Fax: 302-831-3411
					Email: joan@udel.edu, www.chickest.udel.edu.

FEATURES	Location/Qualifiers
source	1..606 /organism="Gallus gallus" /mol_type="mRNA" /db_xref="taxon:9031" /clone="pgnic_pk07_J22" /sex="Male and Female" /tissue_type="thymus, bursa, spleen, PBL, bone marrow" /lab_host="E.coli EMH10B" /clone_lib="normalized chicken lymphoid cDNA library" /note="Vector: pCMVSPORT 6"
ORIGIN	
Alignment Scores:	
Pred. No.:	0.385
Score:	61.00
Percent Similarity:	85.71%
Best Local Similarity:	78.57%
Query Match:	75.31%
DB:	3
AHH26175_COPY_50_65 (1-16) x BQ037883 (1-606)	Length: 606 Matches: 11 Conservative: 1 Mismatches: 2 Indels: 0 Gaps: 0
Qy	1 GluMetThrLeuLysPheGlyProAlaArgAsnSerLysIle 14
Db	268 GAGATGACACTGAATTGTCTGGCTCTGTAATGATGTGTC 309
RESULT 13	
BU662818	BU662818 613 bp mRNA linear EST 30-SEP-2002 LOCUS c19ig01_z1 Hembase; Erythroid Precursor Cells (LCB:c1 library) Homo sapiens cDNA clone c19ig01_5', mRNA sequence.
DEFINITION	
ACCESSION	BU662818
VERSION	BUS
KEYWORDS	GI: 23375003
ORGANISM	Homo sapiens (human)
REFERENCE	1. (bases 1 to 613) Authors Gubin,A.N.,Lee,Y.T.,Bouffard,G.G. and Miller,J.L. Title Gene Expression in Human Erythroid Precursor Cells Journal Unpublished (2002) Comment Contact: Jeffery L. Miller Laboratory of Chemical Biology National Institute of Diabetes and Digestive and Kidney Diseases Building 10, Room 9B17, National Institutes of Health, Bethesda, MD 20892, USA Tel: 301 402 2373 Fax: 301 435 5148 Email: jlm2@nih.gov
COMMENT	The 'cl' library was constructed by Alexander Gubin, Ph.D. in the Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or analyses by National Institutes of Health Intramural Sequencing Center (NIISC). More information available at: http://hembase.nih.gov
FEATURES	Plate: 91 row: 9 column: 01 Seq primer: 5' Lambda-Triplex2 Sequencing Primer.
source	1..613 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="c19ig01" /sex="Unknown" /tissue_type="blood" /cell_type="Erythroid Precursor Cells" /cell_line="Primary Culture of Peripheral Blood Mononuclear Cells" /dev_stage="Precursor erythroblasts; GPA++" /lab_host="RH5Alpha" /clone_lib="Hembase; Erythroid Precursor Cells (LCB:c1
FEATURES	
source	1..621 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells" /clone_lib="GRN_EB" /note="Oligo dT primed, full-length enriched cDNA library from embryoid body outgrowth derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."

library") /note="Organ: blood; Vector: pTRIPLEX2; Site 1: SfiI; Site 2: SfiI; A complementary DNA (cDNA) library from human erythroid precursor cells was constructed using SMART PCR (polymerase chain reaction) cDNA Library Construction Kit (Clontech, Palo Alto, CA) according to the manufacturer's directions, but with slight modifications. Briefly, reverse transcription was performed in the presence of 1 μmol/L peptide nucleic acid (PNA) oligos -biotin-GTC-CGG-AG-CGT-G-(C-terminal) and (N-terminal)-biotin-C(T/C)T-GAA-GTT-CTC-AGG-A-(C-terminal). Synthesized cDNA was digested with SfiI and size-selected on a 1% agarose gel (>800bp). Large-scale sequencing of the library was performed by the NIH Intramural Sequencing Center (NISC); Http://www.nisc.nih.gov/ ."

Search completed: January 12, 2006, 20:45:39
 Job time : 2611 secs

ORIGIN

Alignment Scores:			
Pred. No.:	0.395	Length:	621
Score:	61.00	Matches:	11
Percent Similarity:	85.71%	Conservative:	1
Best Local Similarity:	78.57%	Mismatches:	2
Query Match:	75.31%	Indels:	0
DB:	7	Gaps:	0

AHH26175_COPY_50_65 (1-16) × CN367892 (1-621)

Qy	1 GluMetThrLeuLysPheGlyProAlaArgSerLysIle 14
Db	401 GAGATGACAATCTGAAATTGTGTCCAGCAGTAAATGACAGTGC 442

RESULT 15

AL119505	AL119505	635 bp mRNA linear EST 04-SEP-2003
LOCUS	DKFZP761O191_r1	(synonym: hamy2) Homo sapiens cDNA clone
DEFINITION	DKFZP761O191_5'	mRNA sequence.
ACCESSION	AL119505	
VERSION	AL119505.1	GI:5925404
KEYWORDS	EST	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
Hominidae; Homo		

REFERENCE 1 (bases 1 to 635)

AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and Wiemann,S.

TITLE EST (Ottenwaelder, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

INGOLSTADTER LANDSTR. 1, D-85764 NEUHERBERG, GERMANY

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: S.wiemann@dkfz-heidelberg.de;

sequenced by Medigenomix (Münster(Germany) within the cDNA sequencing consortium of the German Genome Project. No s1 sequence available.

This clone (DKFZP761O191) is available at the RZPD in Berlin.

Please contact the RZPD: Resourcenzentrum Heinberweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source	Organism: "Homo sapiens"
	/mol type="mRNA"
	/db_xref=taxon:9606"
	/clone="DKFZP761O191"
	/tissue_type="amygdala"
	/dev_stage="adult"
	/lab_host="DHB"
	/clone_id="761 (synonym: hamy2)"
	/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN

Alignment Scores:		Length:	635
Pred. No.:	0.406	Matches:	11
Score:	61.00	Conservative:	1
Percent Similarity:	85.71%	Mismatches:	2
Best Local Similarity:	78.57%	Indels:	0
Query Match:	75.31%	Gaps:	0
DB:	1		

AHH26175_COPY_50_65 (1-16) × AL119505 (1-635)

Qy	1 GluMetThrLeuLysPheGlyProAlaArgSerLysIle 14
Db	433 GAGATGACAATCTGAAATTGTGTCCAGCAGTAAATGACAGTGC 474

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OM protein - nucleic search, using frame_plus_P2n model

Run on: January 12, 2006, 18:44:35 ; Search time 141 Seconds
(without alignments)
(201.709 Million cell) updates/sec

Title: AAH26175_COPY_50_65

Pefect Score: 81

Sequence: 1 emtikfpgarnskie 16

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Command line parameters:

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-Q=/cpn2.1/PROTO spool -RAWLINGS1@0076905/runat.10012006.144825.5355/app_query.fasta_1.199
-DB=1 Issued Patents NA -QFMT=fastest -SUFFIX=p2n rni -MINWATCh=0.1 -LOOPCt=0
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blolum62 -TRANS=humn40 .cdi
-LIST=15 -DOALIGN=200 -THR SCORr=pcT -THR MAX=100 -ALIGN=15
-MODE=LOCAL -OUTENT=pcO -NORM=ext -HEAPSzI=500 -MINLEN=0 -MAXLEN=2000000000
-USER=RAWLINGS1@0076905 @CGN_1..1..193 @runat.10012006.144825.5355 -NCPU=6
-DEV TIMEOUT=120 -WARN TIMEOUT=10 -THREADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
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Database : Issued Patents NA:
1: /cgnd_6/podata/1/ina/1_COMB.seq,*
2: /cgnd_6/podata/1/ina/5_COMB.seq,*
3: /cgnd_6/podata/1/ina/6A_COMB.seq,*
4: /cgnd_6/podata/1/ina/6B_COMB.seq,*
5: /cgnd_6/podata/1/ina/H_COMB.seq,*
6: /cgnd_6/podata/1/ina/PCTUS_COMB.seq,*
7: /cgnd_6/podata/1/ina/PP_COMB.seq,*
8: /cgnd_6/podata/1/ina/RE_COMB.seq,*
9: /cgnd_6/podata/1/ina/backfileseq1.seq,*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	61	75.3	1621	3	US-09-103-840A-1	
2	55	67.9	65966	3	US-09-149-016-5410	
3	45	55.6	29604	3	US-09-17152	
4	45	55.6	29604	3	US-09-1767-6315	
5	45	55.6	29604	3	US-09-2270-767-21579	
c 6	45	55.6	1664976	3	US-09-255-991A-637	
c 7	45	55.6	1664976	3	US-09-618-166-207	
c 8	43	53.1	11936	3	US-09-949-016-17428	
9	43	53.1	4403765	3	US-09-103-840A-2	

%

Result No. Score Query Match Length DB ID Description

--

Sequence 1, Appli
Sequence 2916, AP
Sequence 654, APP
Sequence 6315, AP
Sequence 21575, A
Sequence 637, APP
Sequence 616, APP
Sequence 1683, AP
Sequence 9305, AP
Sequence 2641, APP
Sequence 17018, A
Sequence 812, APP
Sequence 15854, A
Sequence 11969, A
Sequence 13238, A
Sequence 11566, A
Sequence 14133, A
Sequence 17100, A
Sequence 1, Appli
Sequence 3318, AP
Sequence 24450, A
Sequence 199833, A
Sequence 9963, AP
Sequence 136, APP
Sequence 8070, AP
Sequence 1265, AP
Sequence 1223, AP
Sequence 2, Appli
Sequence 3, Appli
Sequence 14, Appli
Sequence 1, Appli
Sequence 17, Appli
Sequence 1771, A
Sequence 1262, A
Sequence 17067, A
Sequence 6590, AP

ALIGNMENTS

RESULT 1

US-09-149-016-5410 ; Sequence 5410, Application US/09949016

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIORITY APPLICATION NUMBER: 60/1241,755

; PRIORITY FILING DATE: 2000-10-20

; PRIORITY APPLICATION NUMBER: 60/237,768

; PRIORITY FILING DATE: 2000-10-03

; PRIORITY APPLICATION NUMBER: 60/231,498

; PRIORITY FILING DATE: 2000-09-05

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: Fab-SEQ for Windows Version 4.0

; SEQ ID NO: 5410

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-5410

FEATURE: ;
; NAME/KEY: UNSURE
; LOCATION: 6
; OTHER INFORMATION: Xaa=Pro or Ser
US-09-513-999C-2946

RESULT 2
US-09-949-016-17152
Sequence 17152, Application US/0949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FabSeq For Windows Version 4.0
SEQ ID NO: 17152
LENGTH: 65966
TYPE: DNA
ORGANISM: Human
JS-09-949-016-17152

Alignment Scores:
Pred. No.: 0.132 Length: 65966
Score: 61.10 Matches: 11
Percent Similarity: 85.71% Conservative: 1
Best Local Similarity: 78.57% Mismatches: 2
Query Match: 75.31% Indels: 0
DB: 3 Gaps: 0

AIAH26175_COPY_50_65 (1-16) x US-09-513-999C-2946 (1-229)

RESULT 4
US-08-781-891-207
Sequence 207, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Scheibleberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO WERNER'S SYNDROME
CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES: 209
ADDRESSEE: SED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DBC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Carol
ADDRESS: 6090620enburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
PHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 207:
SEQUENCE CHARACTERISTICS:
LENGTH: 29604 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-781-891-207

Alignment Scores:
Pred. No.: 0.0198 Length: 229
Score: 55.00 Matches: 1.0
Percent Similarity: 78.57% Conservative: 1
Best Local Similarity: 71.43% Mismatches: 3
Query Match: 67.90% Indels: 0
DB: 3 Gaps: 0

AIAH26175_COPY_50_65 (1-16) x US-09-513-999C-2946 (1-229)

RESULT 3
US-09-513-999C-2946
Sequence 2946, Application US/09513999C
Patent No. 6781961
GENERAL INFORMATION:
APPLICANT: Edwards, J. B.
APPLICANT: Duciert, A.
APPLICANT: Giordano, J. Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patient No. 6783561
FILE REFERENCE: 59 US2 REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent .pm
SEQ ID NO: 2946
LENGTH: 229
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 72..227
FEATURE:
NAME/KEY: misc_feature
LOCATION: 87
OTHER INFORMATION: vcf or
DB: 3

Alignment Scores:
Pred. No.: 0.884 Length: 29604
Score: 45.00 Matches: 9
Percent Similarity: 73.33% Conservative: 2
Best Local Similarity: 60.00% Mismatches: 4
Query Match: 55.56% Indels: 0
DB: 3 Gaps: 0

AIAH26175_COPY_50_65 (1-16) x US-08-781-891-207 (1-29604)

Qy 2 MetThrLeuLysPheGlyProAlaArgAsnSerLysIleGluGlu 16
 Db 10506 CTTACCAATTAAAGTTGACCGTAAGAAATAGGGATTTATGAG 10550

RESULT 5
 US-09-618-166-207
 ; Sequence 207, Application US/09618166
 ; GENERAL INFORMATION:
 ; APPLICANT: Yu, Ying-Rui
 ; Oshima, Junko
 ; Mulligan, John T.
 ; Scheilkenberg, Gerald D.
 ; PRODUCTS RELATED TO
 ; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
 ; WERNER'S SYNDROME

NUMBER OF SEQUENCES: 209
 CURRENT APPLICATION NUMBER: 2009
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed Intellectual Property Law Group
 STREET: 701 Fifth Avenue, Suite 6300
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98101-7092

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/618,166
 FILING DATE: 17-Juli-2000
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: McMasters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 240052.419C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 684-6031
 INFORMATION FOR SEQ ID NO: 207:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29604 base pairs
 TYPE: ducleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 207:
 US-09-618-166-207

Alignment Scores:
 pred. No.: 884 Length: 29604
 Score: 4.00 Matches: 9
 Percent Similarity: 73.33% Conservative: 2
 Best Local Similarity: 60.00% Mismatches: 4
 Query Match: 55.56% Indel: 0
 DB: 3 Gaps: 0

AHH26175_COPY_50_65 (1-16) × US-09-618-166-207 (1-29604)
 Qy 2 MetThrLeuLysPheGlyProAlaArgAsnSerLysIleGluGlu 16
 Db 10506 CTTACCAATTAAAGTTGACCGTAAGAAATAGGGATTTATGAG 10550

RESULT 6
 US-09-616-421B-1/C
 ; Sequence 1, Application US/08916421B
 ; GENERAL INFORMATION:
 ; APPLICANT: Bult et al.
 ; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus jannaschii
 ; Pat. No. 6503729
 ; TITLE OF INVENTION: jannaschii

FILE REFERENCE: PB275
 ; CURRENT APPLICATION NUMBER: US/08/916,421B
 ; CURRENT FILING DATE: 1997-08-22
 ; PRIORITY APPLICATION NUMBER: US 60/024,428
 ; PRIORITY FILING DATE: 1996-08-22
 ; NUMBER OF SEQ ID NOS: 3
 ; SEQ ID NO: 1
 ; LENGTH: 1664976
 ; TYPE: DNA
 ; ORGANISM: Methanococcus jannaschii
 ; FEATURES:
 ; NAME/KEY: misc feature
 ; LOCATION: (28222)...(28222)
 ; OTHER INFORMATION: n equals a, t, c, or g
 ; NAME/KEY: misc feature
 ; LOCATION: (28257)...(28258)
 ; OTHER INFORMATION: n equals a, t, c, or g
 ; NAME/KEY: misc feature
 ; LOCATION: (84773)...(84773)
 ; OTHER INFORMATION: n equals a, t, c, or g
 ; NAME/KEY: misc feature
 ; LOCATION: (84808)...(84808)
 ; OTHER INFORMATION: n equals a, t, c, or g
 ; NAME/KEY: misc feature
 ; LOCATION: (84812)...(84812)
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 ; NAME/KEY: misc feature
 ; LOCATION: (101398)...(103998)
 ; OTHER INFORMATION: n equals a, t, c, or g
 ; NAME/KEY: misc feature
 ; LOCATION: (148948)...(148948)
 ; OTHER INFORMATION: n equals a, t, c, or g
 ; NAME/KEY: misc feature
 ; LOCATION: (163395)...(163395)
 ; OTHER INFORMATION: n equals a, t, c, or g
 ; NAME/KEY: misc feature
 ; LOCATION: (191999)...(191999)
 ; OTHER INFORMATION: n equals a, t, c, or g
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 ; OTHER INFORMATION: n equals a, t, c, or g
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 ; LOCATION: (231980)...(231980)
 ; OTHER INFORMATION: n equals a, t, c, or g
 ; NAME/KEY: misc feature
 ; LOCATION: (234814)...(234814)
 ; OTHER INFORMATION: n equals a, t, c, or g
 ; NAME/KEY: misc feature
 ; LOCATION: (309398)...(309398)
 ; OTHER INFORMATION: n equals a, t, c, or g
 ; NAME/KEY: misc_feature

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 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (312837) . (312837)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (312993) . (312993)
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 OTHER INFORMATION: n equals a, t, c, or g
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 NAME/KEY: misc feature
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 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
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 NAME/KEY: misc feature
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 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
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 NAME/KEY: misc feature
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 NAME/KEY: misc feature
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 NAME/KEY: misc feature
 LOCATION: (713652) . (713652)
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 NAME/KEY: misc feature
 LOCATION: (714684) . (714684)
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 NAME/KEY: misc feature
 LOCATION: (779455) . (779455)
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 NAME/KEY: misc feature
 LOCATION: (779676) . (779676)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
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 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (871619) . (871619)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (1084830) . (1084830)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (1109846) . (1096846)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (1119881) . (1119881)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (1310988) . (1310988)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (1313224) . (1313224)
 OTHER INFORMATION: n equals a, t, c, or g
 NAME/KEY: misc feature
 LOCATION: (1349473) . (1349473)

; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1349491) . (1349491)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1470981) . (1470981)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1569020) . (1569020)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1602912) . (1602912)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1603734) . (1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1637998) . (1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1664854) . (1664854)
; OTHER INFORMATION: n equals a, t, c, or g
; US-08-916-421B-1
Alignment Scores:
 Pred. No.: 1.27e+05 Length: 1664976
 Score: 45.00 Matches: 9
 Percent Similarity: 68.75% Conservative: 2
 Best Local Similarity: 56.25% N mismatches: 5
 Query Match: 55.56% Indels: 0
 DB: 3 Gaps: 0

AAH26175_COPY_50_65 (1-16) x US-08-916-421B-1 (1-1664976)

Qy 1 GluMetThrLeuLysPheGlyProAlaArgSerLysIleGluGlu 16
 Db 1471514 GAAATCAAATTAATCAGACCGTTTCGGAAATGAAAGATAAGAA 1471467

RESULT 7
 US 09-692-570-1/C
 ; Sequence 1, Application US/09692570
 ; Patent No. 6797466
 ; GENERAL INFORMATION:
 ; APPLICANT: Bult et al.
 ; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco
 ; Patent No. 6797466
 ; TITLE OF INVENTION: jannaschii
 ; FILE REFERENCE: PB275C1
 ; CURRENT APPLICATION NUMBER: US/09/692,570
 ; CURRENT FILING DATE: 2003-01-14
 ; PRIOR APPLICATION NUMBER: US 60/024,428
 ; PRIOR FILING DATE: 1998-08-22
 ; PRIOR APPLICATION NUMBER: US 08/916,421
 ; PRIOR FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 LENGTH: 1664976
 ; TYPE: DNA
 ; ORGANISM: Methanococcus jannaschii
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (28222) . (28222)
 ; OTHER INFORMATION: n equals a, t, c, or g
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (28257) . (28258)
 ; OTHER INFORMATION: n equals a, t, c, or g
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (84773) . (84773)
 ; OTHER INFORMATION: n equals a, t, c, or g
 ; FEATURE:

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NAME/KEY: misc_feature
LOCATION: (84808) .. (84808)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (84812) .. (84812)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (98120) .. (98120)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (98159) .. (98159)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (98239) .. (98239)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (98266) .. (98266)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (98343) .. (98343)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (103998) .. (103998)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (163385) .. (163385)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (148948) .. (148948)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (191989) .. (191989)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (234187) .. (234187)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (234220) .. (234220)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (234814) .. (234814)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (309398) .. (309398)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (312993) .. (312993)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (319226) .. (319226)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (559167) .. (559167)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (559211) .. (559211)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (600522) .. (600522)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (622798) .. (622798)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (657203) .. (657203)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (674415) .. (674415)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (682442) .. (682442)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (713652) .. (713652)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (779455) .. (779455)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (779676) .. (779676)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (855539) .. (855539)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (871639) .. (871639)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1084830) .. (1084830)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1096846) .. (1096846)

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OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1115881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1130881)..(1130988)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1315224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g

Alignment Scores:
Pred. No.: 1.27e+05 Length: 1664976
Score: 45.00 Matches: 9
Percent Similarity: 68.75% Conservative: 2
Best Local Similarity: 56.25% Mismatches: 5
Query Match: 55.56% Indels: 0
DB: 3 Gaps: 0

AAH26175_COPY_50_65 (1-16) x US-09-692-570-1 (1-1664976)

Qy 1 GluMetThrLeuIysPheGlyProAlaArgAsnSerlysIleGluGlu 16
Db 1471514 GAATCAAAATTAAATCAGACCGTTGGAAATGGAAATGAGAAGAA 1471467

RESULT 8
US-09-949-016-17428
Sequence 17428 Application US/09949016
Patent No. 681339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231, 498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 17428
LENGTH: 11936
TYPE: DNA
ORGANISM: Human
US-09-949-016-17428

Alignment Scores:
Pred. No.: 733 Length: 11936
Score: 43.00 Matches: 8
Percent Similarity: 78.57% Conservative: 3
Best Local Similarity: 57.14% Mismatches: 3
Query Match: 53.09% Indels: 0
DB: 3 Gaps: 0

AAH26175_COPY_50_65 (1-16) x US-09-949-016-17428 (1-11936)

Qy 1 GluMetThrLeuIysPheGlyProAlaArgAsnSerlysIleGluGlu 16

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AAH26175_COPY_50_65 (1-16) x US-09-103-840A-1 (1-4411529)

Qy 4 LeuLysPheGlyProAlaArgLysSerIys 13
Db 3533592 GTCGAAATTAAGCCGGATTGAA 3533621

RESULT 11

US-09-134-000C-2916/c
 Patent No. 6617156
 Sequence 2916, Application US/09134000C
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 032796-032
 CURRENT APPLICATION NUMBER: US/09/134,000C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/055,778
 PRIOR FILING DATE: 1997-08-15
 SEQ ID NOS: 6812
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 2916
 LENGTH: 237
 TYPE: DNA
 ORGANISM: Enterococcus faecalis

Alignment Scores:

Pred. No.:	9.12	Length:	237
Score:	42.00	Matches:	8
Percent Similarity:	73.33%	Conservative:	3
Best Local Similarity:	53.33%	Mismatches:	4
Query Match:	51.85%	Indels:	0
DB:	3	Gaps:	0

AAH26175_COPY_50_65 (1-16) x US-09-134-000C-2916 (1-237)

Qy 2 MetThrLeuLysPheGlyProAlaArgSerLysIleGluGlu 16
 Db 114 ATGTCCACCCCTATGGACCATACCTTAATAACAAAATAGGAA 70

RESULT 12

US-09-252-991A-664
 Sequence 664, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196-136

CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 SEQ ID NO 664
 LENGTH: 450
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa

Alignment Scores:

Pred. No.:	20.2	Length:	450
Score:	42.00	Matches:	8
Percent Similarity:	78.57%	Conservative:	3
Best Local Similarity:	57.14%	Mismatches:	3
Query Match:	51.85%	Indels:	0
DB:	3	Gaps:	0

AAH26175_COPY_50_65 (1-16) x US-09-252-991A-664 (1-450)

Alignment Scores:
 Pred. No.: 20.2
 Score: 42.00
 Percent Similarity: 78.57%
 Best Local Similarity: 57.14%
 Query Match: 51.85%
 DB: 3
 LENGTH: 450
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa

AAH26175_COPY_50_65 (1-16) x US-09-270-767-21597 (1-778)
 Qy 3 ThrLeuLysPheGlyProAlaArgSerIleGluGlu 11
 Db 339 ACACAAAATTGGACCAAGAAAT 313
 RESULT 15
 US-09-252-991A-637
 Sequence 637, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:

Qy 3 ThrLeuLysPheGlyProAlaArgSerIleGluGlu 16
 Db 42 ACCCTGAAATTGGCCGACCTTACGCCAGGCCAAAGAG 83
 RESULT 13
 US-09-270-767-6315/c
 Sequence 6315, Application US/09270767
 ; GENERAL INFORMATION:
 APPLICANT: Homburger et al.
 TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 FILE REFERENCE: File Reference: 7326-094
 CURRENT APPLICATION NUMBER: US/09/270,767
 CURRENT FILING DATE: 1999-03-17
 NUMBER OF SEQ ID NOS: 62517
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 7315
 LENGTH: 778
 TYPE: DNA
 ORGANISM: *Drosophila melanogaster*
 US-09-270-767-6315
 Alignment Scores:
 Pred. No.: 39.8
 Score: 42.00
 Percent Similarity: 88.89%
 Best Local Similarity: 88.89%
 Mismatches: 1
 Indels: 0
 Gaps: 0
 DB:
 AAH26175_COPY_50_65 (1-16) x US-09-270-767-6315 (1-778)
 Qy 3 ThrLeuLysPheGlyProAlaArgSerIleGluGlu 11
 Db 339 ACACAAAATTGGACCAAGAAAT 313
 RESULT 14
 US-09-270-767-21597/c
 Sequence 21597, Application US/09270767
 ; GENERAL INFORMATION:
 APPLICANT: Homburger et al.
 TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 FILE REFERENCE: File Reference: 7326-094
 CURRENT APPLICATION NUMBER: US/09/270,767
 CURRENT FILING DATE: 1999-03-17
 NUMBER OF SEQ ID NOS: 62517
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 21597
 LENGTH: 778
 TYPE: DNA
 ORGANISM: *Drosophila melanogaster*
 US-09-270-767-21597
 Alignment Scores:
 Pred. No.: 39.8
 Score: 42.00
 Percent Similarity: 88.89%
 Best Local Similarity: 88.89%
 Mismatches: 1
 Indels: 0
 Gaps: 0
 DB:
 AAH26175_COPY_50_65 (1-16) x US-09-270-767-21597 (1-778)

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09-252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,150
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS.: 33142
SEQ ID NO: 637
LENGTH: 1407
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-637

Alignment Scores:	Pred. No.:	Score:	Length:
		82.9	1407
		42.00	Matches: 8
		Percent Similarity: 78.57%	Conservative: 3
		Best Local Similarity: 57.14%	Mismatches: 3
		Query Match: 51.85%	Indels: 0
		Db: 3	Gaps: 0

AHH26175_COPY_50_65 (1-16) × US-09-252-991A-637 (1-1407)

Qy 3 ThrIleUlyPheGlyProIlaArgAsnSarLysIleGluGlu 16
Db 1315 ACCCTGCATTGGCCGACCTCAACGCCAGGGAAAGAG 1356

Search completed: January 12, 2006, 21:11:26
Job time : 1545 secs

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